```
Set     Items   Description
S1        328   AU="FIELDS H" OR AU="FIELDS H A"
S2        298   AU="FIELDS H.A." OR AU="FIELDS HA"
S3         75   AU="FIELDS HOWARD" OR AU="FIELDS HOWARD A"
S4        175   AU="KHUDYAKOV Y" OR AU="KHUDYAKOV Y E" OR AU="KHUDYAKOV Y.-
            E." OR AU="KHUDYAKOV YE"
S5         49   AU="KHUDYAKOV YURY" OR AU="KHUDYAKOV YURY E"
S6        733   S1 OR S2 OR S3 OR S4 OR S5
S7      19056   HEPATITIS(W)A(W)VIRUS
S8      14247   HAV
S9      26065   S7 OR S8
S10    543159   VACCINE? ? OR IMMUNOGENIC
S11      1376   P2A
S12       106   S6 AND S7
S13        88   S12 NOT PY>1997
S14        42   RD (unique items)
S15         1   S11 AND S14
S16        10   S14 AND S10
S17        18   S9 AND S10 AND S11
S18        18   S17 NOT PY>2996
S19         6   S18 NOT PY>1997
S20         6   RD (unique items)
?
```

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16/3,AB/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2000 Dialog Corporation. All rts. reserv.

06034651 86200371
Structure of the hepatitis A virion: peptide mapping of the capsid region.
Wheeler CM; Robertson BH; Van Nest G; Dina D; Bradley DW; **Fields HA**
Journal of virology (UNITED STATES) May 1986, 58 (2) p307-13, ISSN 0022-538X Journal Code: KCV
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Milligram amounts of highly purified **hepatitis A virus** (HAV) were obtained from persistently infected cell cultures. The HAV polypeptides were separated by sodium dodecyl sulfate-polyacrylamide gel electrophoresis and transferred to nitrocellulose for detection by an enzyme-linked immunotransfer blot procedure. The HAV nucleotide-derived amino acid sequence was subjected to computer analysis to identify potential **immunogenic** regions within the HAV capsid polypeptides. Synthetic peptides corresponding to selected regions of each of the larger putative capsid polypeptides were coupled to keyhole limpet hemocyanin and used to immunize rabbits. Four of six anti-HAV peptide sera were strongly reactive. Antipeptide serum generated against amino acids (a.a.) 75 through 82 reacted with the 27,000-molecular-weight (MW) polypeptide; serum against a.a. 279 through 285 reacted with the 29,000-MW HAV polypeptide; and sera against a.a. 591 through 602 and 606 through 618 reacted with the 33,000-MW HAV polypeptide. These reactions enabled the identification of the gene order of the larger HAV P1 region gene products. Our data indicate the following molecular weights: HAV VP2 or 1B, 27,000; HAV VP3 or 1C, 29,000; and HAV VP1 or 1D, 33,000.

16/3,AB/3 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs
(c) 2001 Derwent Publ Ltd. All rts. reserv.

0219271 DBA Accession No.: 98-00868 PATENT
Immunogenic hepatitis A virus **peptides- recombinant peptide and DNA sequence**
AUTHOR: **Fields H A ; Khudyakov Y E**
CORPORATE SOURCE: Atlanta, GA, USA.
PATENT ASSIGNEE: U.S.Govt.; U.S.Dep.Health-Hum.Serv.Atlanta 1997
PATENT NUMBER: WO 9740147 PATENT DATE: 971030 WPI ACCESSION NO.: 97-535831 (9749)
PRIORITY APPLIC. NO.: US 15644 APPLIC. DATE: 960419
NATIONAL APPLIC. NO.: WO 97US6891 APPLIC. DATE: 970418
LANGUAGE: English
ABSTRACT: New peptides (72 protein sequences specified) from **immunogenic hepatitis A virus** (HAV) may be used to induce an immune response to HAV in a mammal or to detect the presence of antibodies against HAV in a mammal. DNA sequences encoding the proteins are also claimed, and may be used to produce the recombinant peptides. Some of the claimed peptides can be used to differentiate between **vaccine** -induced immunity and natural immunity. The peptides can also be used to raise antibodies. The peptides are preferably conjugated to a carrier protein chosen from serum albumin, keyhole limpet hemocyanin, diphtheria toxin, tetanus toxin and synthetic polymers. (140pp)

16/3,AB/4 (Item 1 from file: 342)

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DIALOG(R)File 342:Derwent Patents Citation Indx
(c) 2001 Derwent Info Ltd. All rts. reserv.

02989838 WPI Acc No: 97-535831/49
Immunogenic Hepatitis A Virus (HAV) peptide(s) - used to induce an immune response to HAV in a mammal or to detect the presence of antibodies against HAV in a mammal
Patent Assignee: (USSH) US DEPT HEALTH & HUMAN SERVICES
Author (Inventor): **FIELDS H A ; KHUDYAKOV Y E**
Patent (basic)
Patent No Kind Date Examiner Field of Search
WO 9740147 A1 971030 (BASIC)
Derwent Week (Basic): 9749
Priority Data: US 15644 (960419)
Applications: AU 9728103 (970418); WO 97US6891 (970418)
Designated States
(National): AU; CA; JP; US
(Regional): AT; BE; CH; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE
Derwent Class: B04; D16; S03
Int Pat Class: A61K-039/12; C07K-014/10; C12N-015/11
Number of Patents: 002
Number of Countries: 021
Number of Cited Patents: 003
Number of Cited Literature References: 003
Number of Citing Patents: 000

16/3,AB/5 (Item 1 from file: 349)
DIALOG(R)File 349:PCT Fulltext
(c) 2001 WIPO/MicroPat. All rts. reserv.

00538726
ANTIGENICALLY REACTIVE REGIONS OF THE HEPATITIS A VIRUS **POLYPROTEIN REGIONS REACTIVES AUX ANTIGENES DE LA POLYPROTEINE DU VIRUS DE L'HEPATITE A**
Patent Applicant/Assignee:
THE GOVERNMENT OF THE UNITED STATES OF AMERICA represented by THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES Centers for Disease Control and Prevention Technology Transfer Office, THE GOVERNMENT OF THE UNITED STATES OF AMERICA, represented by THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES, Centers for Disease Control and Prevention, Technology Transfer Office , Executive Park, Building 4, Suite 1103, MS E67, Atlanta, GA 30329 , US
Inventor(s):
FIELDS Howard A , FIELDS, Howard, A. , 1823 Jackson Circle Drive, Marietta, GA 30333 , US
KHUDYAKOV Yury E , KHUDYAKOV, Yury E. , 4354 Tremont Court, Duluth, GA 30136 , US
Patent and Priority Information (Country, Number, Date):
Patent: WO 9740147 A1 19971030
Application: WO 97US6891 19970418 (PCT/WO US9706891)
Priority Application: US 9615644 19960419
Designated States: AU CA JP US AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE
Publication Language: English
Filing Language: English
Fulltext Word Count: 33399

English Abstract
The present provides **immunogenic** HAV peptides, antibodies and assays for detecting HAV. **Vaccines** against HAV are also provided.

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French Abstract
Cette invention concerne des peptides du virus de l'hepatite A (VHA) immunogenes, des anticorps et des dosages permettant de detecter le VHA. Des vaccins diriges contre le VHA sont egalement presentes.
?

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20/3,AB/3 (Item 1 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
(c) 2001 AMERICAN CHEMICAL SOCIETY. All rts. reserv.

128012554 CA: 128(2)12554h PATENT
Immunogenic hepatitis A virus peptides, vaccines and antibodies and assays for detection of virus
INVENTOR(AUTHOR): Fields, Howard A.; Khudyakov, Yury E.
LOCATION: USA
ASSIGNEE: United States Dept. of Health and Human Services; Fields, Howard A.; Khudyakov, Yury E.
PATENT: PCT International ; WO 9740147 A1 DATE: 19971030
APPLICATION: WO 97US6891 (19970418) *US 15644 (19960419)
PAGES: 139 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12N-015/11A; C07K-014/10B; A61K-039/12B; G01N-033/576B DESIGNATED COUNTRIES: AU; CA; JP ; US DESIGNATED REGIONAL: AT; BE; CH; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE

20/3,AB/4 (Item 1 from file: 349)
DIALOG(R)File 349:PCT Fulltext
(c) 2001 WIPO/MicroPat. All rts. reserv.

00538726
ANTIGENICALLY REACTIVE REGIONS OF THE HEPATITIS A VIRUS **POLYPROTEIN**
REGIONS REACTIVES AUX ANTIGENES DE LA POLYPROTEINE DU VIRUS DE L'HEPATITE A
Patent Applicant/Assignee:
THE GOVERNMENT OF THE UNITED STATES OF AMERICA represented by THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES Centers for Disease Control and Prevention Technology Transfer Office, THE GOVERNMENT OF THE UNITED STATES OF AMERICA, represented by THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES, Centers for Disease Control and Prevention, Technology Transfer Office , Executive Park, Building 4, Suite 1103, MS E67, Atlanta, GA 30329 , US
Inventor(s):
FIELDS Howard A, FIELDS, Howard, A. , 1823 Jackson Circle Drive, Marietta, GA 30333 , US
KHUDYAKOV Yury E, KHUDYAKOV, Yury E. , 4354 Tremont Court, Duluth, GA 30136 , US
Patent and Priority Information (Country, Number, Date):
Patent: WO 9740147 A1 19971030
Application: WO 97US6891 19970418 (PCT/WO US9706891)
Priority Application: US 9615644 19960419
Designated States: AU CA JP US AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE
Publication Language: English
Filing Language: English
Fulltext Word Count: 33399

English Abstract
The present provides **immunogenic HAV** peptides, antibodies and assays for detecting **HAV** . **Vaccines** against **HAV** are also provided.

French Abstract
Cette invention concerne des peptides du virus de l'hepatite A (VHA) immunogenes, des anticorps et des dosages permettant de detecter le VHA. Des vaccins diriges contre le VHA sont egalement presentes.

20/3,AB/5 (Item 2 from file: 349)

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DIALOG(R)File 349:PCT Fulltext
(c) 2001 WIPO/MicroPat. All rts. reserv.

00356498

RECOMBINANT VIRUS IMMUNOTHERAPY

IMMUNOTHERAPIE PAR VIRUS RECOMBINE

Patent Applicant/Assignee:
VIROGENETICS CORPORATION
Inventor(s):
PAOLETTI Enzo
TARTAGLIA James
COX William I

Patent and Priority Information (Country, Number, Date):
Patent: WO 9416716 A1 19940804
Application: WO 94US888 19940121 (PCT/WO US9400888)
Priority Application: US 937115 19930121; US 94184009 19940119
Designated States: AU CA JP AT BE CH DE DK ES FR GB GR IE IT LU MC NL PT SE
Publication Language: English
Fulltext Word Count: 52601

English Abstract
Attenuated recombinant viruses containing DNA coding for a cytokine and/or a tumor associated antigen, as well as methods and compositions employing the viruses, are disclosed and claimed. The recombinant viruses can be NYVAC or ALVAC recombinant viruses. The DNA can code for at least one of: human tumor necrosis factor; nuclear phosphoprotein p53, wildtype or mutant; human melanoma-associated antigen; IL-2; IFNgamma; IL-4; GMCSF; IL-12; B7; erb-B-2 and carcinoembryonic antigen. The recombinant viruses and gene products therefrom are useful for cancer therapy.

Japanese Abstract
Des virus recombines attenues contenant l'ADN codant pour un antigene associe a une cytokine ou a une tumeur sont decrits et revendiques, ainsi que des procedes d'utilisation de ces virus et des compositions les comprenant. Les virus recombines peuvent etre des virus NYVAC (virus de la **vaccine**) ou ALVAC (virus de la variole aviaire). L'ADN peut coder pour au moins l'un des elements suivants: le facteur de necrose tumorale humain, la phosphoproteine nucleaire p53, de phenotype sauvage ou mutant; l'antigene associe au melanome humain; l'interleukine- 2 (IL-2); l'interferon gamma (IFNgamma); IL-4; le facteur stimulant les colonies de granulocytes macrophages; IL-12; B7; l'antigene carcinoembryonnaire et erb-B-2. Ces virus recombines et les produits geniques qui en sont derives peuvent etre utilises pour la therapie du cancer.

?

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2001, 16:21:02 ; Search time 121.9 Seconds
(without alignments)
9.379 Million cell updates/sec

Title: US-09-171-432A-39
Perfect score: 107
Sequence: 1 SHIECRKPYKELRLEVGKQR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0401:*
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2: /SIDS1/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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6: /SIDS1/gcgdata/geneseq/geneseqp/AA1985.DAT:*
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22: /SIDS1/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	107	100.0	20	18	W42922	Immunogenic Hepati
2	107	100.0	366	6	P50230	Sequence of hepati
3	107	100.0	854	6	P50287	Sequence encoded b
4	107	100.0	993	6	P50116	Sequence of Hepati
5	107	100.0	993	6	P50231	Sequence encoded b
6	107	100.0	1077	20	W95559	A partial hepatiti
7	107	100.0	1091	14	R32426	Translated from 5'
8	107	100.0	2227	11	R05697	Attenuated hepatit
9	107	100.0	2227	18	W34074	Hepatitis A virus
10	107	100.0	2227	21	B18607	Amino acid sequenc
11	107	100.0	2227	21	B18608	Amino acid sequenc
12	107	100.0	2227	21	B18609	Amino acid sequenc
13	91	85.0	2227	7	P60066	Sequence of viral
14	84.5	79.0	839	12	R15629	Capsid region of c
15	67	62.6	20	18	W42923	Immunogenic Hepati
16	44	41.1	71	21	G07411	Arabidopsis thalia
17	44	41.1	88	21	G61775	Arabidopsis thalia
18	44	41.1	346	12	R11068	12D3 antigen seque
19	43	40.2	287	21	G06838	Arabidopsis thalia
20	43	40.2	312	21	G06837	Arabidopsis thalia
21	43	40.2	320	21	G06836	Arabidopsis thalia
22	43	40.2	391	8	P70479	Sequence of the ma
23	43	40.2	391	13	R25305	HRSV major capsid
24	43	40.2	391	19	W50001	HRSV major nucleoc
25	42.5	39.7	5405	16	W14749	IgG-Fc binding pro
26	41	38.3	66	21	B42172	Human ORFX ORF1936
27	41	38.3	80	21	Y72099	Human serine prote
28	41	38.3	96	17	W03670	HIV-1 strain MAD,
29	41	38.3	112	21	Y91641	Human secreted pro
30	41	38.3	144	21	G08483	Arabidopsis thalia
31	41	38.3	153	21	G08482	Arabidopsis thalia
32	41	38.3	160	20	Y59898	Human normal pancr
33	41	38.3	162	21	G08481	Arabidopsis thalia
34	41	38.3	254	21	B08937	Human secreted pro
35	41	38.3	265	22	B63707	Human gastric canc
36	41	38.3	315	21	B08902	Human secreted pro
37	41	38.3	324	21	B08939	Human secreted pro
38	41	38.3	391	13	R24184	Bovine RSV strain
39	41	38.3	397	13	R21328	Sequence of protei
40	41	38.3	445	21	Y84897	A human proliferat
41	41	38.3	492	20	Y41686	Human PRO274 prote
42	41	38.3	492	21	B44242	Human PRO274 (UNQ2
43	41	38.3	507	21	G40932	Zea mays protein f
44	41	38.3	568	21	G40931	Zea mays protein f
45	41	38.3	568	21	Y94927	Human secreted pro

ALIGNMENTS

RESULT 1
W42922
ID W42922 standard; peptide; 20 AA.
XX
AC W42922;
XX
DT 28-APR-1998 (first entry)
XX
DE Immunogenic Hepatitis A virus peptide YK-1315.
XX
KW Immunogenic peptide; immunogenic epitope; P2A protein;
KW immune response; antibody.
XX
OS Synthetic.
OS Hepatitis A virus.
XX
PN WO9740147-A1.
XX
PD 30-OCT-1997.
XX
PF 18-APR-1997; 97WO-US06891.
XX
PR 19-APR-1996; 96US-0015644.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Fields HA, Khudyakov YE;
XX
DR WPI; 1997-535831/49.
XX
PT Immunogenic Hepatitis A Virus (HAV) peptide(s) - used to induce an
PT immune response to HAV in a mammal or to detect the presence of
PT antibodies against HAV in a mammal
XX

```
PS   Claim 18; Page 112; 140pp; English.
XX
CC   Peptides W42922-30 are immunogenic peptides corresponding to immunogenic
CC   epitopes of the Hepatitis A virus (HAV). The peptides are substantially
CC   similar to a portion of the amino acid sequence of the P2A protein of HAV
CC   corresponding to amino acids 792-980. The present peptide is derived
CC   from amino acids 792-811, and has a reactivity of 54.2% with acute sera.
CC   Compositions containing the peptides can be used to induce an immune
CC   response to HAV in a mammal. The peptides can also be used to detect the
CC   presence of antibodies against HAV in mammalian serum. The peptides can
CC   also be used to make an antibody against HAV by administering the peptide
CC   to a mammal.
XX
SQ   Sequence   20 AA;


  Query Match             100.0%;  Score 107;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-10;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db      1 shiecrkpykelrlevgkqr 20


RESULT   2
P50230
ID   P50230 standard; Protein; 366 AA.
XX
AC   P50230;
XX
DT   28-NOV-1991  (first entry)
XX
DE   Sequence of hepatitis A virus (HAV) surface protein (VP-1).
XX
KW   Hepatitis A virus vaccine; immunisation; monoclonal antibody;
KW   diagnostic assay.
XX
OS   Hepatitis A virus.
XX
PN   EP138704-A.
XX
PD   24-APR-1985.
XX
PF   09-OCT-1984;   84EP-0402025.
XX
PR   02-MAR-1984;   84US-0585942.
PR   14-OCT-1983;   83US-0541836.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Hughes JV,  Scolnick EM,  Tomassini JE;
XX
DR   WPI; 1985-100818/17.
DR   N-PSDB; N50274.
XX
PT   New hepatitis A virus surface protein - useful for binding to
PT   neutralising antibodies to the virus
XX
PS   Claim 21; Page 46-48; 49pp; English.
XX
CC   VP1 is isolated by solubilisation of the intact virus in an aq.
CC   anionic surfactant and a reducing agent. The viral proteins are sepd.
CC   and the protein of molecular wt. 33000 daltons is sepd.
XX
SQ   Sequence   366 AA;


  Query Match             100.0%;  Score 107;  DB 6;  Length 366;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db    301 shiecrkpykelrlevgkqr 320


RESULT   3
P50287
ID   P50287 standard; Protein; 854 AA.
XX
AC   P50287;
XX
DT   30-NOV-1991  (first entry)
XX
DE   Sequence encoded by hepatitis A virus (HAV) cDNA from near the
DE   genome 5' terminus to the end of the area corresponding to the
DE   capsid protein region of poliovirus RNA.
XX
KW   Hepatitis A virus assay; antigen; antibody.
XX
OS   Hepatitis A virus.
XX
PN   WO8501517-A.
XX
PD   11-APR-1985.
XX
PF   27-SEP-1984;   84WO-US01552.
XX
PR   30-SEP-1983;   83US-0537911.
XX
PA   (MASI ) MASSACHUSETTS INST TECH.
XX
PI   Ticechurst JR,  Baltimore D,  Feinstone SM,  Purcell RH;
PI   Racaniello VR;
XX
DR   WPI; 1985-098846/16.
DR   N-PSDB; N50330.
XX
PT   New hepatitis A virus CDNA - useful in assays for the virus and
PT   for prodn. of the viral antigen and antibodies to it
XX
PS   Example; Fig 7; 60pp; English.
XX
CC   The inventors claim HAV cDNA and a method for producing it, whereby
CC   large amts. can be obtd. economically. The cDNA is useful in the
CC   assay for detection of HAV quickly and easily and with high
CC   sensitivity and specificity. The HAV cDNA is also used in the prodn.
CC   of HAV antigen or antibodies to it. The antibodies may be monoclonal.
XX
SQ   Sequence   854 AA;


  Query Match             100.0%;  Score 107;  DB 6;  Length 854;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db    792 shiecrkpykelrlevgkqr 811


RESULT   4
P50116
ID   P50116 standard; Protein; 993 AA.
XX
AC   P50116;
XX
DT   30-SEP-1991  (first entry)
XX
DE   Sequence of Hepatitis A virus (HAV) immunogenic peptides
DE   VP-1, VP-2, VP-3 and VP-4.
XX
KW   Antigenic protein; immunogen; vaccine.
XX
OS   Hepatitis A virus (strain CR326).
```

XX
PN EP154587-A.
XX
PD 11-SEP-1985.
XX
PF 27-FEB-1985; 85EP-0400369.
XX
PR 02-MAR-1984; 84US-0585818.
XX
PA (MERI) MERCK & CO INC.
XX
PI Linemeyer DL, Menke JG, Reuben RG, Mitra SW;
XX
DR WPI; 1985-224964/37.
DR N-PSDB; N50139.
XX
PT New nucleotide sequences coding for hepatitis A virus antigens -
PT useful for eliciting normal immune response and in vaccines for
PT protecting against the virus
XX
PS Example; Page 11-17; 32pp; English.
XX
CC Within the sequence in N50139 is encoded the information necessary
CC to make the antigenic proteins of HAV. The sequences encoding for
CC the structural proteins begin at base 403. The key sub-unit
CC sequences within VP-1, designated Sequences I,II,III,IV, and V,
CC start, respectively at 1882, 1963, 1999, 2146, 2347. Other
CC nucleotide sequences which are valuable as encoding antigenic
CC proteins are the sequences from base 1749 to base 2722; from base
CC 1487 to base 2980 and from base 1644 to base 2722. The sequence from
CC base 1749 to base 2722 is esp. valuable as a vector for producing
CC antigen protein. Sequences II-V are claimed. X in P50116 denotes the
CC translation of a stop codon.
XX
SQ Sequence 993 AA;

Query Match 100.0%; Score 107; DB 6; Length 993;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SHIECRKPYKELRLEVGKQR 20
||||||||||||||||||||
Db 928 shiecrkpykelrlevgkqr 947

RESULT 5
P50231
ID P50231 standard; Protein; 993 AA.
XX
AC P50231;
XX
DT 28-NOV-1991 (first entry)
XX
DE Sequence encoded by partial sequence of hepatitis A virus (HAV),
DE including surface protein (VP-1).
XX
KW Hepatitis A virus vaccine; immunisation; monoclonal antibody;
KW diagnostic assay.
XX
OS Hepatitis A virus.
XX
FH Key Location/Qualifiers
FT Protein 628..993
FT /note= "claimed; X denotes translated stop codons
FT and unspecified triplets"
XX
PN EP138704-A.
XX
PD 24-APR-1985.
XX
PF 09-OCT-1984; 84EP-0402025.
XX
PR 02-MAR-1984; 84US-0585942.
PR 14-OCT-1983; 83US-0541836.
XX
PA (MERI) MERCK & CO INC.
XX
PI Hughes JV, Scolnick EM, Tomassini JE;
XX
DR WPI; 1985-100818/17.
DR N-PSDB; N50274.
XX
PT New hepatitis A virus surface protein - useful for binding to
PT neutralising antibodies to the virus
XX
PS Disclosure; Page 17-23; 49pp; English.
XX
CC VP1 is isolated by solubilisation of the intact virus in an aq.
CC anionic surfactant and a reducing agent. The viral proteins are sepd.
CC and the protein of molecular wt. 33000 daltons is sepd.
XX
SQ Sequence 993 AA;

Query Match 100.0%; Score 107; DB 6; Length 993;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SHIECRKPYKELRLEVGKQR 20
||||||||||||||||||||
Db 928 shiecrkpykelrlevgkqr 947

RESULT 6
W95559
ID W95559 standard; Protein; 1077 AA.
XX
AC W95559;
XX
DT 28-APR-1999 (first entry)
XX
DE A partial hepatitis A virus (HAV) protein.
XX
KW Hepatitis A virus protein; HAV; P2 region;
KW cell-culture-adapted HAV strain; infection; accelerated growth.
XX
OS Hepatitis A virus.
XX
PN US5849562-A.
XX
PD 15-DEC-1998.
XX
PF 06-JUN-1995; 95US-0468926.
XX
PR 06-NOV-1991; 91US-0788262.
PR 30-SEP-1983; 83US-0537911.
PR 27-SEP-1984; 84US-0654942.
PR 06-OCT-1988; 88US-0256135.
PR 06-JUN-1995; 95US-0468926.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Emerson SU, Purcell RH;
XX
DR WPI; 1999-094412/08.
DR N-PSDB; X01006.
XX
PT Chimeric hepatitis A virus strains - with P2 region from
PT cell-culture-adapted strain in wild-type genome
XX
PS Disclosure; Fig 7A-L; 36pp; English.
XX
CC The present sequence represents a partial hepatitis A virus (HAV)
CC protein. The specification describes a DNA construct consisting
CC of a wild-type HAV genome in which the P2 region is replaced by the

```
CC   P2 region from a cell-culture-adapted HAV strain. The construct is
CC   used to demonstrate that mutations in the P2 region of a
CC   cell-culture-adapted HAV strain are sufficient for establishment of
CC   infection and accelerated growth in cell culture.
XX
SQ   Sequence   1077 AA;


  Query Match             100.0%;  Score 107;  DB 20;  Length 1077;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db   1015 shiecrkpykelrlevgkqr 1034


RESULT   7
R32426
ID   R32426 standard; Protein; 1091 AA.
XX
AC   R32426;
XX
DT   10-JUN-1993  (first entry)
XX
DE   Translated from 5' region of Hepatitis A Virus genomic clone.
XX
KW   HAV HM-175; chronic liver disease; picornavirus.
XX
OS   Hepatitis A Virus.
XX
FH   Key             Location/Qualifiers
FT   Region          238..1091
FT                   /label= ORF
FT                   /note= "second putative initiation codon at
FT                          position 240"
FT   Region          1..711
FT                   /note= "X's correspond to nonsense codons,
FT                          i.e. this region is not an ORF"
XX
PN   US7788262-A.
XX
PD   15-DEC-1992.
XX
PF   30-SEP-1983;   83US-0536911.
XX
PR   27-SEP-1984;   84US-0654942.
PR   06-OCT-1988;   88US-0256135.
PR   30-SEP-1983;   83US-0536911.
PR   06-NOV-1991;   91US-0788262.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX
PI   Baltimore D,  Feinstone SM;
PI    Purcell RH,  Racaniello VR,  Ticehurst JR;
XX
DR   WPI; 1993-067429/08.
DR   N-PSDB; Q36934.
XX
PT   Hepatitis A virus cDNA prodn. - for diagnostic use and for prodn.
PT   of antigen and antibodies
XX
PS   Disclosure; Fig 7; 65pp; English.
XX
CC   HAV virion RNA was extracted from the livers of marmosets which had
CC   been inoculated with HAV (the HAV had previously been passaged twice
CC   in marmosets). The RNA was used to prepare ds cDNA clones by
CC   standard methods. Clones contg. inserts which hybridised to RNA from
CC   HAV-infected African Green Monkey Kidney cells were selected for
CC   further analysis. A 7.4kb restriction map (about 99% of the HAV
CC   genome) was constructed from 5 overlapping inserts. The sequence of
CC   the first 3.3kb (approx.) from the 5'-terminus was determined. An
CC   amino acid sequence was decoded from the entire clone and an open
CC   reading frame was identified starting at position 238. A comparison
CC   of the predicted HAV amino acid sequences with the known capsid
CC   protein sequences of other picornaviruses (poliovirus, foot and
CC   mouth disease virus and encephalomyelitis virus) revealed areas of
CC   local homology.
XX
SQ   Sequence   1091 AA;


  Query Match             100.0%;  Score 107;  DB 14;  Length 1091;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db   1029 shiecrkpykelrlevgkqr 1048


RESULT   8
R05697
ID   R05697 standard; protein; 2227 AA.
XX
AC   R05697;
XX
DT   15-AUG-1990  (first entry)
XX
DE   Attenuated hepatitis A virus.
XX
KW   Hepatitis A virus; vaccine; attenuated.
XX
OS   Hepatitis A virus, strain HM-175.
XX
FH   Key             Location/Qualifiers
FT   Region          1..23
FT                   /label=VP4 = 1A
FT   Region          24..245
FT                   /label=VP2 = 1B
FT   Region          246..491
FT                   /label=VP3 = 1C
FT   Region          492..791
FT                   /label=VP1 = 1D
FT   Region          792..980
FT                   /label=2A
FT   Region          981..1087
FT                   /label=2B
FT   Region          1088..1422
FT                   /label=2C
FT   Region          1423..1496
FT                   /label=3A
FT   Region          1497..1519
FT                   /label=3B = VPg
FT   Region          1520..1738
FT                   /label=3C
FT   Region          1739..2227
FT                   /label=3D
XX
PN   US4894228-A.
XX
PD   16-JAN-1990.
XX
PF   12-JUL-1988;   88US-0217824.
XX
PR   12-JUL-1988;   88US-0217824.
PR   12-JUL-1988;   88US-0652967.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN.
XX
PI   Purcell RH,  Ticehurst JR,  Cohen I,  Emerson SU,  Feinstone SM;
PI   Daemer RJ,  Gust ID;
XX
DR   WPI; 1990-075557/10.
DR   N-PSDB; Q03512.
XX
```

```
PT   Vaccine against hepatitis A virus  infection -  comprises novel
PT   attenuated hepatitis A virus strain.
XX
PS   Claim 1; Fig 1; 18pp; English.
XX
CC   The attenuated HAV is useful for inducing protective immunity against
CC   HAV. This strain (Pass 35) differs from the wild type HAV HM-175 by
CC   several nucleotide changes distributed throughout the genome, is
CC   attenuated for chimpanzees, elicits serum neutralising antibodies, and is
CC   suitable for use as an HAV vaccine. It is noted that not all the changes
CC   are necessary for attenuation and use as a vaccine.
XX
SQ   Sequence   2227 AA;


  Query Match             100.0%;  Score 107;  DB 11;  Length 2227;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db    792 shiecrkpykelrlevgkqr 811


RESULT   9
W34074
ID   W34074 standard; Protein; 2227 AA.
XX
AC   W34074;
XX
DT   27-APR-1998  (first entry)
XX
DE   Hepatitis A virus HM-175 protein sequence.
XX
KW   HAV; attenuation; 2C protein; 2C chimeric hepatitis A virus;
KW   infection; vaccine.
XX
OS   Hepatitis A virus HM-175.
XX
FH   Key             Location/Qualifiers
FT   Protein         1..23
FT                   /label= VP4
FT   Protein         24..245
FT                   /label= VP2
FT   Protein         246..491
FT                   /label= VP3
FT   Protein         492..791
FT                   /label= VP1
FT   Protein         792..980
FT                   /label= 2A
FT   Protein         981..1087
FT                   /label= 2B
FT   Protein         1088..1422
FT                   /label= 2C
FT   Protein         1423..1496
FT                   /label= 3A
FT   Protein         1497..1519
FT                   /label= 3B
FT   Protein         1520..1738
FT                   /label= 3C
FT   Protein         1739..2227
FT                   /label= 3D
XX
PN   WO9740166-A2.
XX
PD   30-OCT-1997.
XX
PF   18-APR-1997;   97WO-US06506.
XX
PR   19-APR-1996;   96US-0015642.
XX
PA   (USSH ) US SEC DEPT HEALTH.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Emerson SU,  Purcell RH,  Raychaudhuri G;
XX
DR   WPI; 1997-535850/49.
DR   N-PSDB; T93023.
XX
PT   Human attenuated HAV genome containing simian HAV 2C gene - useful
PT   as vaccines against HAV infection
XX
PS   Disclosure; Fig 13A-D; 66pp; English.
XX
CC   This protein sequence is encoded by the human hepatitis A virus
CC   (HAV) HM-175 wild-type genome (see T93023).  Attenuated strain
CC   HAV/7 is obtained by passage of HM-175 in African Green Monkey
CC   kidney cells.  A claimed DNA construct (I) comprises a genome of
CC   HAV, where the genome is a human attenuated HAV genome in which a
CC   region of the 2C gene has been replaced by a corresponding region
CC   from a 2C gene of a simian AGM-27 HAV genome (see T93024).  The
CC   region of the 2C gene from AGM-27 contained in the construct
CC   preferably encodes amino acids 120-328 of the 2C protein, amino
CC   acids 1-121 or amino acids 1-328.  Also claimed are: (1) an RNA
CC   transcript of (I); (2) a cell transfected with (I) or the RNA
CC   transcript of (1); (3) a HAV genome as above; (4) antibodies to the
CC   HAV of (3); and (5) a host cell containing the HAV of (3).  (I) or
CC   its RNA transcript, can be used as a vaccine for preventing HAV in
CC   a mammal.  (I) or the RNA transcript can also be used to stimulate
CC   the production of protective antibodies in the mammal.
XX
SQ   Sequence   2227 AA;


  Query Match             100.0%;  Score 107;  DB 18;  Length 2227;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db    792 shiecrkpykelrlevgkqr 811


RESULT  10
B18607
ID   B18607 standard; Protein; 2227 AA.
XX
AC   B18607;
XX
DT   15-JAN-2001  (first entry)
XX
DE   Amino acid sequence of wild type Hepatitis A virus strain HM-175.
XX
KW   HAV; strain HM-174; MRC-5 cell; live vaccine; hepatitis A infection.
XX
OS   Hepatitis A virus.
XX
PN   US6113912-A.
XX
PD   05-SEP-2000.
XX
PF   07-JUN-1995;   95US-0475886.
XX
PR   18-SEP-1992;   92US-0947338.
PR   17-SEP-1993;   93WO-US08610.
PR   10-MAR-1995;   95US-0397232.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   D'Hondt E,  Purcell RH,  Emerson SU,  Funkhouser AW;
XX
DR   WPI; 2000-586464/55.
DR   N-PSDB; A75476.
XX
PT   Novel live hepatitis A virus adapted to growth in human fibroblast cell
PT   line useful as vaccine for protecting humans against hepatitis A virus
```

```
PT   infection, has modified genome compared to wild type  -
XX
PS   Disclosure; Fig 6A-K; 72pp; English.
XX
CC   The present sequence is derived from a wild type hepatitis A virus
CC   (HAV) strain HM-174. The sequence is modified to produce HAV which
CC   are adapted to growth in the human fibroblast-like cell line MRC-5.
CC   The HAV is able to propagate in MRC-5 cells and retain appropriate
CC   attenuation. It is useful as a live vaccine for prophylaxis of
CC   hepatitis A in humans and other primates.
XX
SQ   Sequence   2227 AA;


  Query Match            100.0%;  Score 107;  DB 21;  Length 2227;
  Best Local Similarity  100.0%;  Pred. No. 4.8e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db    792 shiecrkpykelrlevgkqr 811


RESULT  11
B18608
ID   B18608 standard; Protein; 2227 AA.
XX
AC   B18608;
XX
DT   15-JAN-2001  (first entry)
XX
DE   Amino acid sequence of passage 35 Hepatitis A virus called P-35.
XX
KW   HAV; strain HM-174; MRC-5 cell; live vaccine; hepatitis A infection;
KW   P-35 virus.
XX
OS   Hepatitis A virus.
XX
PN   US6113912-A.
XX
PD   05-SEP-2000.
XX
PF   07-JUN-1995;   95US-0475886.
XX
PR   18-SEP-1992;   92US-0947338.
PR   17-SEP-1993;   93WO-US08610.
PR   10-MAR-1995;   95US-0397232.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   D'Hondt E,  Purcell RH,  Emerson SU,  Funkhouser AW;
XX
DR   WPI; 2000-586464/55.
DR   N-PSDB; A75477.
XX
PT   Novel live hepatitis A virus adapted to growth in human fibroblast cell
PT   line useful as vaccine for protecting humans against hepatitis A virus
PT   infection, has modified genome compared to wild type  -
XX
PS   Disclosure; Columns 67-78; 72pp; English.
XX
CC   The present sequence is derived from passage 35 of a wild type
CC   hepatitis A virus (HAV) strain HM-174. The resulting virus is
CC   designated P-35 virus. The sequence is modified to produce HAV which
CC   are adapted to growth in the human fibroblast-like cell line MRC-5.
CC   The HAV is able to propagate in MRC-5 cells and retain appropriate
CC   attenuation. It is useful as a live vaccine for prophylaxis of
CC   hepatitis A in humans and other primates.
XX
SQ   Sequence   2227 AA;


  Query Match            100.0%;  Score 107;  DB 21;  Length 2227;
  Best Local Similarity  100.0%;  Pred. No. 4.8e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db    792 shiecrkpykelrlevgkqr 811


RESULT  12
B18609
ID   B18609 standard; Protein; 2227 AA.
XX
AC   B18609;
XX
DT   15-JAN-2001  (first entry)
XX
DE   Amino acid sequence of live attenuated Hepatitis A virus 4380.
XX
KW   HAV; strain HM-174; MRC-5 cell; live vaccine; hepatitis A infection;
KW   HAV 4380.
XX
OS   Hepatitis A virus.
XX
PN   US6113912-A.
XX
PD   05-SEP-2000.
XX
PF   07-JUN-1995;   95US-0475886.
XX
PR   18-SEP-1992;   92US-0947338.
PR   17-SEP-1993;   93WO-US08610.
PR   10-MAR-1995;   95US-0397232.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   D'Hondt E,  Purcell RH,  Emerson SU,  Funkhouser AW;
XX
DR   WPI; 2000-586464/55.
DR   N-PSDB; A75478.
XX
PT   Novel live hepatitis A virus adapted to growth in human fibroblast cell
PT   line useful as vaccine for protecting humans against hepatitis A virus
PT   infection, has modified genome compared to wild type  -
XX
PS   Disclosure; Columns 93-104; 72pp; English.
XX
CC   The present sequence is derived from a live attenuated hepatitis A
CC   virus (HAV) of the invention, designated HAV 4380. The sequence is
CC   produced by modifying wild type HAV strain HM-174. The HAV of the
CC   invention are adapted to growth in the human fibroblast-like cell
CC   line MRC-5. The HAV is able to propagate in MRC-5 cells and retain
CC   appropriate attenuation. It is useful as a live vaccine for prophylaxis
CC   of hepatitis A in humans and other primates.
XX
SQ   Sequence   2227 AA;


  Query Match            100.0%;  Score 107;  DB 21;  Length 2227;
  Best Local Similarity  100.0%;  Pred. No. 4.8e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db    792 shiecrkpykelrlevgkqr 811


RESULT  13
P60066
ID   P60066 standard; Protein; 2227 AA.
XX
AC   P60066;
XX
DT   26-JUN-1991  (first entry)
```

```
XX
DE   Sequence of viral L434 polypeptide encoded by the complete
DE   nucleotide sequence of the HAV genome.
XX
KW   Diagnosis; vaccine; passive immunotherapy.
XX
OS   Hepatitis A virus.
XX
FH   Key             Location/Qualifiers
FT   Region          1..245
FT                   /label= P1.1A
FT   Region          246..491
FT                   /label= 1B
FT   Region          492..836
FT                   /label= 1C
FT   Region          837..980
FT                   /label= P2.2A
FT   Region          981..1076
FT                   /label= 2B
FT   Region          1077..1422
FT                   /label= 2C
FT   Region          1423..1484
FT                   /label= P3.3A
FT   Region          1485..1507
FT                   /label= 3B
FT   Region          1508..1678
FT                   /label= 3C
FT   Region          1679..2227
FT                   /label= 3D
XX
PN   EP199480-A.
XX
PD   29-OCT-1986.
XX
PF   03-APR-1986;   86EP-0302465.
XX
PR   03-APR-1985;   85US-0719329.
XX
PA   (CHIR-) CHIRON CORP.
XX
PI   Dina D,  Potter SJ,  Vannest GA,  Caput D;
XX
DR   WPI; 1986-286213/44.
DR   N-PSDB; N60080.
XX
PT   Hepatitis A virus nucleotide sequence and polypeptide - and use
PT   in prodn. of vaccines and diagnostic probes
XX
PS   Claim 5; Fig 1; 18pp; English.
XX
CC   N60080 and oligonucleotide fragments are useful in detection of
CC   hepatitis A virus; transformed hosts may be used for expression of
CC   polypeptides and fragments useful in vaccines without risk of
CC   infection by the virus or in prodn. of particles which are capable
CC   of inducing immmunocompetent B cells for passive immunotherapy. Pref.
CC   epitope is derived from AAs 445-657 or 792-848 of the HAV
CC   polypeptide sequence (P60066).
XX
SQ   Sequence   2227 AA;


  Query Match             85.0%;  Score 91;  DB 7;  Length 2227;
  Best Local Similarity   85.0%;  Pred. No. 1.5e-05;
  Matches   17;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 SHIECRKPYKELRLEVGKQR 20
           :||| |||||||||:|||||
Db     792 thiesrkpykelrlqvgkqr 811


RESULT  14
R15629
ID   R15629 standard; Protein; 839 AA.
XX
AC   R15629;
XX
DT   17-MAR-1992  (first entry)
XX
DE   Capsid region of cyno-HAV isolate CY-145.
XX
KW   Hepatitis A virus; cynomolgus; HAV; monkey; vaccine; macaque.
XX
OS   Cynomolgus monkey hepatitis A virus, isolate CY-145.
XX
FH   Key             Location/Qualifiers
FT   Protein         1..245
FT                   /label= VP0
FT   Protein         246..491
FT                   /label= VP3
FT   Protein         492..791
FT                   /label= VP1
FT   Protein         792
FT                   /label= P2
FT                   /note= "incomplete"
FT   Cleavage-site   245..246
FT   Cleavage-site   491..492
FT   Cleavage-site   791..792
FT   Active-site     315
FT   Active-site     593
XX
PN   US7678828-A.
XX
PD   12-NOV-1991.
XX
PF   03-APR-1991;   91US-0678828.
XX
PR   03-APR-1991;   91US-0678828.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN.
XX
PI   Hainan OV,  Margolis HS,  Robertson BH,  Brinton MH,  Ebert JW;
XX
DR   WPI; 1991-376737/51.
DR   N-PSDB; Q15180.
XX
PT   Hepatitis A virus isolates and DNA - used to prepare vaccines for
PT   preventing hepatitis A virus infection.
XX
PS   Disclosure; Fig 3; 23pp; English.
XX
CC   The sequence was deduced from the nucleotide sequence obtd. by PCR
CC   amplification of cyno-HAV viral RNA obtd. from the stool of a
CC   cynomolgus monkey with serologically and histologically confirmed
CC   spontaneous hepatitis A. The sequence differs from the  human HAV
CC   isolate HM175 (Cohen, J.I., et al. (1987) Proc. Natl. Acad. Sci.
CC   USA 84, 2497-2501), mainly in the VP3 and VP1 proteins. The Gln-Val
CC   pair at the VP3-VP1 cleavage site in the human isolate is replaced
CC   by a Gln-Thr pair in the cyno-HAV.The other two cleavage sites are
CC   the same.  Two residues have been identified as part of the immuno-
CC   dominant region (see feature table) and are different to those in
CC   the same position in human HAV. The protein and peptides derived
CC   from it can be used in the prepn. of vaccines for the prevention of
CC   HAV infection.
CC   See also R15056.
XX
SQ   Sequence   839 AA;


  Query Match             79.0%;  Score 84.5;  DB 12;  Length 839;
  Best Local Similarity   90.0%;  Pred. No. 5.5e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    1;  Gaps    1;

Qy       1 SHIECRKPYKELRLEVGKQR 20
           |||| :|||||||||||||||
Db     792 shie-kkpykelrlevgkqr 810
```

```
RESULT  15
W42923
ID   W42923 standard; peptide; 20 AA.
XX
AC   W42923;
XX
DT   28-APR-1998  (first entry)
XX
DE   Immunogenic Hepatitis A virus peptide YK-1316.
XX
KW   Immunogenic peptide; immunogenic epitope; P2A protein;
KW   immune response; antibody.
XX
OS   Synthetic.
OS   Hepatitis A virus.
XX
PN   WO9740147-A1.
XX
PD   30-OCT-1997.
XX
PF   18-APR-1997;   97WO-US06891.
XX
PR   19-APR-1996;   96US-0015644.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Fields HA,  Khudyakov YE;
XX
DR   WPI; 1997-535831/49.
XX
PT   Immunogenic Hepatitis A Virus (HAV) peptide(s) - used to induce an
PT   immune response to HAV in a mammal or to detect the presence of
PT   antibodies against HAV in a mammal
XX
PS   Claim 18; Page 112; 140pp; English.
XX
CC   Peptides W42922-30 are immunogenic peptides corresponding to immunogenic
CC   epitopes of the Hepatitis A virus (HAV). The peptides are substantially
CC   similar to a portion of the amino acid sequence of the P2A protein of HAV
CC   corresponding to amino acids 792-980. The present peptide is derived
CC   from amino acids 799-818, and has a reactivity of 41.7% with acute sera.
CC   Compositions containing the peptides can be used to induce an immune
CC   response to HAV in a mammal. The peptides can also be used to detect the
CC   presence of antibodies against HAV in mammalian serum. The peptides can
CC   also be used to make an antibody against HAV by administering the peptide
CC   to a mammal.
XX
SQ   Sequence   20 AA;


  Query Match             62.6%;  Score 67;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.00058;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       8 PYKELRLEVGKQR 20
           |||||||||||||
Db       1 pykelrlevgkqr 13


Search completed: April 24, 2001, 16:23:11
Job time: 129 sec
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OM protein - protein search, using sw model

Run on: April 24, 2001, 16:23:39 ; Search time 113.97 Seconds
(without alignments)
20.568 Million cell updates/sec

Title: US-09-171-432A-39
Perfect score: 107
Sequence: 1 SHIECRKPYKELRLEVGKQR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	107	100.0	56	14	Q67818	Q67818 hepatitis a
2	107	100.0	56	14	Q67819	Q67819 hepatitis a
3	107	100.0	56	14	Q67820	Q67820 hepatitis a
4	107	100.0	56	14	Q67821	Q67821 hepatitis a
5	107	100.0	56	14	Q67822	Q67822 hepatitis a
6	107	100.0	56	14	Q67823	Q67823 hepatitis a
7	107	100.0	56	14	O39865	O39865 hepatitis a
8	107	100.0	56	14	O39866	O39866 hepatitis a
9	107	100.0	56	14	O39867	O39867 hepatitis a
10	107	100.0	56	14	O39868	O39868 hepatitis a
11	107	100.0	56	14	O39869	O39869 hepatitis a
12	107	100.0	56	14	O39870	O39870 hepatitis a
13	107	100.0	56	14	O39871	O39871 hepatitis a
14	107	100.0	56	14	O39872	O39872 hepatitis a
15	107	100.0	56	14	O39873	O39873 hepatitis a
16	107	100.0	56	14	O39874	O39874 hepatitis a
17	107	100.0	56	14	Q96829	Q96829 hepatitis a
18	107	100.0	56	14	Q9QP08	Q9qp08 hepatitis a
19	107	100.0	56	14	Q9IPD2	Q9ipd2 hepatitis a
20	107	100.0	56	14	Q9IPD1	Q9ipd1 hepatitis a
21	107	100.0	56	14	Q9IPC9	Q9ipc9 hepatitis a
22	107	100.0	56	14	Q9IPC8	Q9ipc8 hepatitis a
23	107	100.0	56	14	Q9IPC7	Q9ipc7 hepatitis a
24	107	100.0	56	14	Q9IPC5	Q9ipc5 hepatitis a
25	107	100.0	56	14	Q9IPC4	Q9ipc4 hepatitis a
26	107	100.0	56	14	Q9IPC2	Q9ipc2 hepatitis a
27	107	100.0	56	14	Q9IPC1	Q9ipc1 hepatitis a
28	107	100.0	56	14	Q9IPC0	Q9ipc0 hepatitis a
29	107	100.0	56	14	Q9IPB9	Q9ipb9 hepatitis a
30	107	100.0	56	14	Q9IPB7	Q9ipb7 hepatitis a
31	107	100.0	56	14	Q9IPB6	Q9ipb6 hepatitis a
32	107	100.0	56	14	Q9IPB5	Q9ipb5 hepatitis a
33	107	100.0	56	14	Q9IPB4	Q9ipb4 hepatitis a
34	107	100.0	56	14	Q9IPB3	Q9ipb3 hepatitis a
35	107	100.0	56	14	Q9IPB2	Q9ipb2 hepatitis a
36	107	100.0	56	14	Q9IPB1	Q9ipb1 hepatitis a
37	107	100.0	56	14	Q9IPB0	Q9ipb0 hepatitis a
38	107	100.0	56	14	Q9IPA9	Q9ipa9 hepatitis a
39	107	100.0	56	14	Q9IPA8	Q9ipa8 hepatitis a
40	107	100.0	56	14	Q9IPA7	Q9ipa7 hepatitis a
41	107	100.0	56	14	Q9IPA5	Q9ipa5 hepatitis a
42	107	100.0	56	14	Q9IPA4	Q9ipa4 hepatitis a
43	107	100.0	56	14	Q9IPA3	Q9ipa3 hepatitis a
44	107	100.0	56	14	Q9IPA2	Q9ipa2 hepatitis a
45	107	100.0	56	14	Q9IPA1	Q9ipa1 hepatitis a

ALIGNMENTS

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RESULT   1
Q67818
ID   Q67818      PRELIMINARY;      PRT;    56 AA.
AC   Q67818;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENTS).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ISR-05, AFULA DISTRICT, ISRAEL, 1993;
RA   Karetnyi Y.V., Shulman L.M., Manor J., Leitner L., Shehab S.,
RA   Mendelson E.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77243; CAB01036.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein; Nonstructural protein.
FT   NON_TER       1      1
FT   CHAIN         1     >28       CAPSID PROTEIN VP1.
FT   NON_CONS     28     29
FT   CHAIN        29     >56       NONSTRUCTURAL PROTEIN NS2A.
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;


  Query Match             100.0%;  Score 107;  DB 14;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 SHIECRKPYKELRLEVGKQR 20
           ||||||||||||||||||||
Db      29 SHIECRKPYKELRLEVGKQR 48


RESULT   2
Q67819
ID   Q67819      PRELIMINARY;      PRT;    56 AA.
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AC   Q67819;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENTS).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ISR-10, (AFULA DISTRICT, ISRAEL, 1993);
RA   Karetnyi Y.V., Shulman L.M., Manor J., Leitner L., Shehab S.,
RA   Mendelson E.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77244; CAB01037.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein; Nonstructural protein.
FT   NON_TER       1      1
FT   CHAIN         1    >28       CAPSID PROTEIN VP1.
FT   NON_CONS     28     29
FT   CHAIN        29    >56       NONSTRUCTURAL PROTEIN NS2A.
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;

  Query Match            100.0%;  Score 107;  DB 14;  Length 56;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db     29 SHIECRKPYKELRLEVGKQR 48


RESULT   3
Q67820
ID   Q67820      PRELIMINARY;      PRT;    56 AA.
AC   Q67820;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENTS).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ISR-12, (AFULA DISTRICT, ISRAEL, 1993);
RA   Karetnyi Y.V., Shulman L.M., Manor J., Leitner L., Shehab S.,
RA   Mendelson E.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77245; CAB01038.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein; Nonstructural protein.
FT   NON_TER       1      1
FT   CHAIN         1    >28       CAPSID PROTEIN VP1.
FT   NON_CONS     28     29
FT   CHAIN        29    >56       NONSTRUCTURAL PROTEIN NS2A.
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;

  Query Match            100.0%;  Score 107;  DB 14;  Length 56;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db     29 SHIECRKPYKELRLEVGKQR 48


RESULT   4
Q67821
ID   Q67821      PRELIMINARY;      PRT;    56 AA.
AC   Q67821;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENTS).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ISR-15, (AFULA DISTRICT, ISRAEL, 1993);
RA   Karetnyi Y.V., Shulman L.M., Manor J., Leitner L., Shehab S.,
RA   Mendelson E.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77246; CAB01039.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein; Nonstructural protein.
FT   NON_TER       1      1
FT   CHAIN         1    >28       CAPSID PROTEIN VP1.
FT   NON_CONS     28     29
FT   CHAIN        29    >56       NONSTRUCTURAL PROTEIN NS2A.
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;

  Query Match            100.0%;  Score 107;  DB 14;  Length 56;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db     29 SHIECRKPYKELRLEVGKQR 48


RESULT   5
Q67822
ID   Q67822      PRELIMINARY;      PRT;    56 AA.
AC   Q67822;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENTS).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ISR-70, (AKKO DISTRICT, ISRAEL, 1993);
RA   Karetnyi Y.V., Shulman L.M., Manor J., Leitner L., Shehab S.,
RA   Mendelson E.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77247; CAB01040.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein; Nonstructural protein.
FT   NON_TER       1      1
FT   CHAIN         1    >28       CAPSID PROTEIN VP1.
FT   NON_CONS     28     29
FT   CHAIN        29    >56       NONSTRUCTURAL PROTEIN NS2A.
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;

  Query Match            100.0%;  Score 107;  DB 14;  Length 56;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-09;
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db     29 SHIECRKPYKELRLEVGKQR 48


RESULT   6
Q67823
ID   Q67823      PRELIMINARY;      PRT;    56 AA.
AC   Q67823;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENTS).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ISR-79, (AKKO DISTRICT, ISRAEL, 1993);
RA   Karetnyi Y.V., Shulman L.M., Manor J., Leitner L., Shehab S.,
RA   Mendelson E.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77248; CAB01041.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein; Nonstructural protein.
FT   NON_TER       1      1
FT   CHAIN         1    >28       CAPSID PROTEIN VP1.
FT   NON_CONS     28     29
FT   CHAIN        29    >56       NONSTRUCTURAL PROTEIN NS2A.
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;


  Query Match             100.0%;  Score 107;  DB 14;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db     29 SHIECRKPYKELRLEVGKQR 48


RESULT   7
O39865
ID   O39865      PRELIMINARY;      PRT;    56 AA.
AC   O39865;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENT).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=412991;
RX   MEDLINE=97247817; PubMed=9093940;
RA   Taylor M.B.;
RT   "Molecular epidemiology of South African strains of hepatitis A virus:
RT   1982-1996.";
RL   J. Med. Virol. 51:273-279(1997).
DR   EMBL; U68689; AAB53585.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein.
FT   NON_TER       1      1
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;


  Query Match             100.0%;  Score 107;  DB 14;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db     29 SHIECRKPYKELRLEVGKQR 48


RESULT   8
O39866
ID   O39866      PRELIMINARY;      PRT;    56 AA.
AC   O39866;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENT).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=96001190;
RX   MEDLINE=97247817; PubMed=9093940;
RA   Taylor M.B.;
RT   "Molecular epidemiology of South African strains of hepatitis A virus:
RT   1982-1996.";
RL   J. Med. Virol. 51:273-279(1997).
DR   EMBL; U68690; AAB53586.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein.
FT   NON_TER       1      1
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;


  Query Match             100.0%;  Score 107;  DB 14;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db     29 SHIECRKPYKELRLEVGKQR 48


RESULT   9
O39867
ID   O39867      PRELIMINARY;      PRT;    56 AA.
AC   O39867;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENT).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JVR;
RX   MEDLINE=97247817; PubMed=9093940;
RA   Taylor M.B.;
RT   "Molecular epidemiology of South African strains of hepatitis A virus:
RT   1982-1996.";
RL   J. Med. Virol. 51:273-279(1997).
DR   EMBL; U68692; AAB53588.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein.
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FT   NON_TER       1      1
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;


  Query Match             100.0%;  Score 107;  DB 14;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db     29 SHIECRKPYKELRLEVGKQR 48


RESULT  10
O39868
ID   O39868      PRELIMINARY;      PRT;    56 AA.
AC   O39868;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENT).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=503712;
RX   MEDLINE=97247817; PubMed=9093940;
RA   Taylor M.B.;
RT   "Molecular epidemiology of South African strains of hepatitis A virus:
RT   1982-1996.";
RL   J. Med. Virol. 51:273-279(1997).
DR   EMBL; U68693; AAB53589.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein.
FT   NON_TER       1      1
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;


  Query Match             100.0%;  Score 107;  DB 14;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db     29 SHIECRKPYKELRLEVGKQR 48


RESULT  11
O39869
ID   O39869      PRELIMINARY;      PRT;    56 AA.
AC   O39869;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENT).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=96002382;
RX   MEDLINE=97247817; PubMed=9093940;
RA   Taylor M.B.;
RT   "Molecular epidemiology of South African strains of hepatitis A virus:
RT   1982-1996.";
RL   J. Med. Virol. 51:273-279(1997).
DR   EMBL; U68694; AAB53590.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein.
FT   NON_TER       1      1
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;


  Query Match             100.0%;  Score 107;  DB 14;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db     29 SHIECRKPYKELRLEVGKQR 48


RESULT  12
O39870
ID   O39870      PRELIMINARY;      PRT;    56 AA.
AC   O39870;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENT).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=406808;
RX   MEDLINE=97247817; PubMed=9093940;
RA   Taylor M.B.;
RT   "Molecular epidemiology of South African strains of hepatitis A virus:
RT   1982-1996.";
RL   J. Med. Virol. 51:273-279(1997).
DR   EMBL; U68695; AAB53591.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein.
FT   NON_TER       1      1
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6642 MW;  465CF51846AEF4BC CRC64;


  Query Match             100.0%;  Score 107;  DB 14;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db     29 SHIECRKPYKELRLEVGKQR 48


RESULT  13
O39871
ID   O39871      PRELIMINARY;      PRT;    56 AA.
AC   O39871;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENT).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=923359;
RX   MEDLINE=97247817; PubMed=9093940;
RA   Taylor M.B.;
RT   "Molecular epidemiology of South African strains of hepatitis A virus:
```

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RT   1982-1996.";
RL   J. Med. Virol. 51:273-279(1997).
DR   EMBL; U68696; AAB53592.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein.
FT   NON_TER       1      1
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6642 MW;  465CF51846AEF4BC CRC64;


  Query Match             100.0%;  Score 107;  DB 14;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db     29 SHIECRKPYKELRLEVGKQR 48


RESULT  14
O39872
ID   O39872      PRELIMINARY;      PRT;    56 AA.
AC   O39872;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENT).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VDM;
RX   MEDLINE=97247817; PubMed=9093940;
RA   Taylor M.B.;
RT   "Molecular epidemiology of South African strains of hepatitis A virus:
RT   1982-1996.";
RL   J. Med. Virol. 51:273-279(1997).
DR   EMBL; U68697; AAB53593.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein.
FT   NON_TER       1      1
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6642 MW;  465CF51846AEF4BC CRC64;


  Query Match             100.0%;  Score 107;  DB 14;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db     29 SHIECRKPYKELRLEVGKQR 48


RESULT  15
O39873
ID   O39873      PRELIMINARY;      PRT;    56 AA.
AC   O39873;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENT).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=2333;
RX   MEDLINE=97247817; PubMed=9093940;
RA   Taylor M.B.;
RT   "Molecular epidemiology of South African strains of hepatitis A virus:
RT   1982-1996.";
RL   J. Med. Virol. 51:273-279(1997).
DR   EMBL; U68698; AAB53594.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein.
FT   NON_TER       1      1
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;


  Query Match             100.0%;  Score 107;  DB 14;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db     29 SHIECRKPYKELRLEVGKQR 48


Search completed: April 24, 2001, 16:33:07
Job time: 568 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2001, 16:24:44 ; Search time 38.74 Seconds
(without alignments)
17.685 Million cell updates/sec

Title: US-09-171-432A-39
Perfect score: 107
Sequence: 1 SHIECRKPYKELRLEVGKQR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	107	100.0	341	1	POLG_HPAV1	P13672 hepatitis a
2	107	100.0	852	1	POLG_HPAVC	P06442 hepatitis a
3	107	100.0	2226	1	POLG_HPAV2	P26580 hepatitis a
4	107	100.0	2226	1	POLG_HPAV4	P26581 hepatitis a
5	107	100.0	2226	1	POLG_HPAV8	P26582 hepatitis a
6	107	100.0	2227	1	POLG_HPAVH	P08617 hepatitis a
7	107	100.0	2227	1	POLG_HPAVL	P06441 hepatitis a
8	107	100.0	2227	1	POLG_HPAVM	P13901 hepatitis a
9	95	88.8	808	1	POLG_HPAVG	Q02381 hepatitis a
10	86	80.4	2230	1	POLG_HPAVS	P14553 simian hepa
11	84.5	79.0	839	1	POLG_HPAVT	P31788 simian hepa
12	46	43.0	420	1	YAGA_SCHPO	Q09873 schizosacch
13	43.5	40.7	1663	1	CO3_RAT	P01026 rattus norv
14	43	40.2	391	1	NCAP_HRSV1	P24566 human respi
15	42	39.3	210	1	LOLA_XYLFA	Q9pdc7 xylella fas
16	42	39.3	286	1	PU91_SCICO	P22311 sciara copr
17	42	39.3	723	1	SYM_PYRHO	O58721 pyrococcus
18	42	39.3	861	1	TOP1_BUCAI	P57371 buchnera ap
19	41	38.3	319	1	URED_SYNPV	O87399 synechococc
20	41	38.3	364	1	SUCC_METJA	Q57663 methanococc
21	41	38.3	370	1	T2M2_METJA	Q58844 methanococc
22	41	38.3	391	1	NCAP_BRSV3	P35943 bovine resp
23	41	38.3	391	1	NCAP_BRSVA	P22677 bovine resp
24	41	38.3	391	1	NCAP_BRSVR	Q65708 bovine resp
25	41	38.3	391	1	NCAP_HRSVA	P03418 human respi
26	41	38.3	4543	1	LRP1_CHICK	P98157 gallus gall
27	41	38.3	4544	1	LRP1_HUMAN	Q07954 homo sapien
28	40.5	37.9	141	1	V16K_TRVTC	P05076 tobacco rat
29	40.5	37.9	1120	1	RPOM_SCHPO	O13993 schizosacch
30	40.5	37.9	1663	1	CO3_MOUSE	P01027 mus musculu
31	40.5	37.9	2198	1	YLJ2_CAEEL	P34367 caenorhabdi
32	40	37.4	69	1	MOP_HAEIN	P45183 haemophilus
33	40	37.4	309	1	US16_HCMVA	P09717 human cytom
34	40	37.4	345	1	EFB1_MOUSE	P52795 mus musculu
35	40	37.4	391	1	NCAP_ORSVW	Q83957 ovine respi
36	40	37.4	458	1	NIFK_CLOPA	P11347 clostridium
37	40	37.4	558	1	Y369_MYCPN	P75231 mycoplasma
38	40	37.4	1017	1	DPOL_ADEB2	O72539 bovine aden
39	40	37.4	3432	1	POLG_JAEV1	P27395 j genome po
40	40	37.4	3432	1	POLG_JAEV5	P19110 j genome po
41	40	37.4	3432	1	POLG_JAEVJ	P32886 j genome po
42	39.5	36.9	422	1	POLS_RRV2	P17517 ross river
43	39	36.4	141	1	GAT3_YEAST	Q07928 saccharomyc
44	39	36.4	177	1	CYSC_SYNY3	P72940 synechocyst
45	39	36.4	236	1	VEAD_BPP22	Q03546 bacteriopha

ALIGNMENTS

RESULT 1
POLG_HPAV1
ID POLG_HPAV1 STANDARD; PRT; 341 AA.
AC P13672;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP3; CORE PROTEIN
DE P2A] (FRAGMENT).
OS Hepatitis A virus (strain LCDC-1).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Hepatovirus.
OX NCBI_TaxID=12093;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89263805; PubMed=2542903;
RA Andonov A.P., Lau P., Chaudhary R.;
RT "Nucleotide sequence of the VP1 gene from a Chinese strain of
RT hepatitis A virus (HAV).";
RL Nucleic Acids Res. 17:3594-3594(1989).
CC -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC ---
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CC ---
DR EMBL; X14666; CAA32794.1; -.
DR PIR; S04137; S04137.
KW Polyprotein; Coat protein; Core protein.
FT NON_TER 1 1
FT CHAIN <1 1 COAT PROTEIN VP3 (1C).
FT CHAIN 2 340 COAT PROTEIN VP1 (1D).
FT CHAIN 341 >341 CORE PROTEIN P2A.
FT NON_TER 341 341
SQ SEQUENCE 341 AA; 38003 MW; 066918289BF126D5 CRC64;

Query Match 100.0%; Score 107; DB 1; Length 341;
Best Local Similarity 100.0%; Pred. No. 4.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SHIECRKPYKELRLEVGKQR 20
||||||||||||||||||||
Db 296 SHIECRKPYKELRLEVGKQR 315

RESULT 2
POLG_HPAVC
ID POLG_HPAVC STANDARD; PRT; 852 AA.

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AC   P06442; Q83741; Q83742;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEIN
DE   P2A] (FRAGMENT).
OS   Hepatitis A virus (strain CR326).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12097;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85185648; PubMed=2985793;
RA   Linemeyer D.L., Menke J.G., Martin-Gallardo A., Hughes J.V.,
RA   Young A., Mitra S.W.;
RT   "Molecular cloning and partial sequencing of hepatitis A viral cDNA.";
RL   J. Virol. 54:247-255(1985).
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M10033; AAA45470.1; -.
DR   PIR; A03904; GNNYHA.
KW   Polyprotein; Coat protein; Core protein.
FT   CHAIN         1     23       COAT PROTEIN VP4 (P1A).
FT   CHAIN        24    245       COAT PROTEIN VP2 (P1B).
FT   CHAIN       246    491       COAT PROTEIN VP3 (P1C).
FT   CHAIN       492    836       COAT PROTEIN VP1 (P1D).
FT   CHAIN       837   >852       CORE PROTEIN P2A.
FT   NON_TER     852    852
SQ   SEQUENCE   852 AA;  95563 MW;  73D3ED0AD532820E CRC64;


  Query Match             100.0%;  Score 107;  DB 1;  Length 852;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 SHIECRKPYKELRLEVGKQR 20
           ||||||||||||||||||||
Db     792 SHIECRKPYKELRLEVGKQR 811


RESULT   3
POLG_HPAV2
ID   POLG_HPAV2     STANDARD;      PRT;  2226 AA.
AC   P26580;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
DE   P2A TO P2C; PROBABLE PROTEINS P3A TO P3C; RNA-DIRECTED RNA POLYMERASE
DE   P3D (EC 2.7.7.48)].
OS   Hepatitis A virus (strain 24a).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12094;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91162758; PubMed=1705995;
RA   Lemon S.M., Murphy P.C., Shields P.A., Ping L.H., Feinstone S.M.,
RA   Cromeans T., Jansen R.W.;
RT   "Antigenic and genetic variation in cytopathic hepatitis A virus
RT   variants arising during persistent infection: evidence for genetic
RT   recombination.";
RL   J. Virol. 65:2056-2065(1991).
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M59810; AAA45468.1; -.
DR   MEROPS; C03.005; -.
DR   InterPro; IPR000605; -.
DR   InterPro; IPR001205; -.
DR   Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR   Pfam; PF00910; RNA_helicase; 1.
KW   Polyprotein; Coat protein; Core protein; Transferase;
KW   RNA-directed RNA polymerase; Hydrolase; Thiol protease.
FT   CHAIN         1     23       COAT PROTEIN VP4 (P1A).
FT   CHAIN        24    245       COAT PROTEIN VP2 (P1B).
FT   CHAIN       246    491       COAT PROTEIN VP3 (P1C).
FT   CHAIN       492    794       COAT PROTEIN VP1 (P1D).
FT   CHAIN       795    900       CORE PROTEIN P2A.
FT   CHAIN       901   1087       CORE PROTEIN P2B.
FT   CHAIN      1088   1422       CORE PROTEIN P2C.
FT   CHAIN      1423   1495       PROBABLE PROTEIN P3A.
FT   CHAIN      1496   1518       PROBABLE PROTEIN P3B.
FT   CHAIN      1519   1737       PROBABLE PROTEIN P3C.
FT   CHAIN      1738   2226       RNA-DIRECTED POLYMERASE P3D.
SQ   SEQUENCE   2226 AA;  251152 MW;  6CD85A91D6B4E2BF CRC64;


  Query Match             100.0%;  Score 107;  DB 1;  Length 2226;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 SHIECRKPYKELRLEVGKQR 20
           ||||||||||||||||||||
Db     792 SHIECRKPYKELRLEVGKQR 811


RESULT   4
POLG_HPAV4
ID   POLG_HPAV4     STANDARD;      PRT;  2226 AA.
AC   P26581;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
DE   P2A TO P2C; PROBABLE PROTEINS P3A TO P3C; RNA-DIRECTED RNA POLYMERASE
DE   P3D (EC 2.7.7.48)].
OS   Hepatitis A virus (strain 43c).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12095;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91162758; PubMed=1705995;
RA   Lemon S.M., Murphy P.C., Shields P.A., Ping L.H., Feinstone S.M.,
RA   Cromeans T., Jansen R.W.;
RT   "Antigenic and genetic variation in cytopathic hepatitis A virus
RT   variants arising during persistent infection: evidence for genetic
RT   recombination.";
RL   J. Virol. 65:2056-2065(1991).
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
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CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
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CC   ---------------------------------------------------------------------
DR   EMBL; M59809; AAA45469.1; -.
DR   MEROPS; C03.005; -.
DR   InterPro; IPR000605; -.
DR   InterPro; IPR001205; -.
DR   Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR   Pfam; PF00910; RNA_helicase; 1.
KW   Polyprotein; Coat protein; Core protein; Transferase;
KW   RNA-directed RNA polymerase; Hydrolase; Thiol protease.
FT   CHAIN         1     23       COAT PROTEIN VP4 (P1A).
FT   CHAIN        24    245       COAT PROTEIN VP2 (P1B).
FT   CHAIN       246    491       COAT PROTEIN VP3 (P1C).
FT   CHAIN       492    794       COAT PROTEIN VP1 (P1D).
FT   CHAIN       795    900       CORE PROTEIN P2A.
FT   CHAIN       901   1087       CORE PROTEIN P2B.
FT   CHAIN      1088   1422       CORE PROTEIN P2C.
FT   CHAIN      1423   1495       PROBABLE PROTEIN P3A.
FT   CHAIN      1496   1518       PROBABLE PROTEIN P3B.
FT   CHAIN      1519   1737       PROBABLE PROTEIN P3C.
FT   CHAIN      1738   2226       RNA-DIRECTED POLYMERASE P3D.
SQ   SEQUENCE   2226 AA;  251107 MW;  403B4CA80B09BF75 CRC64;


  Query Match             100.0%;  Score 107;  DB 1;  Length 2226;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db    792 SHIECRKPYKELRLEVGKQR 811


RESULT   5
POLG_HPAV8
ID   POLG_HPAV8     STANDARD;      PRT;  2226 AA.
AC   P26582;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
DE   P2A TO P2C; PROBABLE PROTEINS P3A TO P3C; RNA-DIRECTED RNA POLYMERASE
DE   P3D (EC 2.7.7.48)].
OS   Hepatitis A virus (strain 18f).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12096;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91162758; PubMed=1705995;
RA   Lemon S.M., Murphy P.C., Shields P.A., Ping L.H., Feinstone S.M.,
RA   Cromeans T., Jansen R.W.;
RT   "Antigenic and genetic variation in cytopathic hepatitis A virus
RT   variants arising during persistent infection: evidence for genetic
RT   recombination.";
RL   J. Virol. 65:2056-2065(1991).
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
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CC   ---------------------------------------------------------------------
DR   EMBL; M59808; AAA45467.1; -.
DR   MEROPS; C03.005; -.
DR   InterPro; IPR000605; -.
DR   InterPro; IPR001205; -.
DR   Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR   Pfam; PF00910; RNA_helicase; 1.
KW   Polyprotein; Coat protein; Core protein; Transferase;
KW   RNA-directed RNA polymerase; Hydrolase; Thiol protease.
FT   CHAIN         1     23       COAT PROTEIN VP4 (P1A).
FT   CHAIN        24    245       COAT PROTEIN VP2 (P1B).
FT   CHAIN       246    491       COAT PROTEIN VP3 (P1C).
FT   CHAIN       492    794       COAT PROTEIN VP1 (P1D).
FT   CHAIN       795    900       CORE PROTEIN P2A.
FT   CHAIN       901   1087       CORE PROTEIN P2B.
FT   CHAIN      1088   1422       CORE PROTEIN P2C.
FT   CHAIN      1423   1495       PROBABLE PROTEIN P3A.
FT   CHAIN      1496   1518       PROBABLE PROTEIN P3B.
FT   CHAIN      1519   1737       PROBABLE PROTEIN P3C.
FT   CHAIN      1738   2226       RNA-DIRECTED POLYMERASE P3D.
SQ   SEQUENCE   2226 AA;  251292 MW;  24964A63396C8D6B CRC64;


  Query Match             100.0%;  Score 107;  DB 1;  Length 2226;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db    792 SHIECRKPYKELRLEVGKQR 811


RESULT   6
POLG_HPAVH
ID   POLG_HPAVH     STANDARD;      PRT;  2227 AA.
AC   P08617; P06443; Q81082;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
DE   P2A TO P2C; PROBABLE PROTEINS P3A TO P3C; RNA-DIRECTED RNA POLYMERASE
DE   P3D (EC 2.7.7.48)].
OS   Hepatitis A virus (strain HM-175).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12098;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WILD TYPE;
RX   MEDLINE=87061253; PubMed=3023706;
RA   Cohen J.I., Ticehurst J.R., Purcell R.H., Buckler-White A.,
RA   Baroudy B.M.;
RT   "Complete nucleotide sequence of wild-type hepatitis A virus:
RT   comparison with different strains of hepatitis A virus and other
RT   picornaviruses.";
RL   J. Virol. 61:50-59(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATTENUATED;
RX   MEDLINE=87175701; PubMed=3031686;
RA   Cohen J.I., Rosenblum B., Ticehurst J.R., Daemer R.J., Feinstone S.M.,
RA   Purcell R.H.;
RT   "Complete nucleotide sequence of an attenuated hepatitis A virus:
RT   comparison with wild-type virus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:2497-2501(1987).
RN   [3]
RP   SEQUENCE OF 1-854 AND 1724-2227 FROM N.A.
RX   MEDLINE=85166289; PubMed=2984684;
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RA   Baroudy B.M., Ticehurst J.R., Miele T.A., Maizel J.V. Jr.,
RA   Purcell R.H., Feinstone S.M.;
RT   "Sequence analysis of hepatitis A virus cDNA coding for capsid
RT   proteins and RNA polymerase.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:2143-2147(1985).
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- MISCELLANEOUS: STRAIN HM-175/7 MK-5 IS ATTENUATED STRAIN DERIVED
CC       FROM HM-175 BY 32 PASSAGES IN AFRICAN GREEN MONKEY KIDNEY CELLS.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC   -!- CAUTION: REF.3 SEQUENCE HAS A NUMBER OF CONFLICTS WITH THAT
CC       SHOWN.
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M14114; AAA45475.1; -.
DR   EMBL; M14707; AAA45465.1; -.
DR   EMBL; M14707; AAA45466.1; ALT_INIT.
DR   EMBL; M16632; AAA45471.1; -.
DR   PIR; A25981; GNNYHM.
DR   PIR; A25914; GNNYMK.
DR   PIR; A03905; A03905.
DR   MEROPS; C03.005; -.
DR   InterPro; IPR000605; -.
DR   InterPro; IPR001205; -.
DR   Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR   Pfam; PF00910; RNA_helicase; 1.
KW   Polyprotein; Coat protein; Core protein; Transferase;
KW   RNA-directed RNA polymerase; Hydrolase; Thiol protease.
FT   CHAIN         1     23       COAT PROTEIN VP4 (P1A).
FT   CHAIN        24    245       COAT PROTEIN VP2 (P1B).
FT   CHAIN       246    491       COAT PROTEIN VP3 (P1C).
FT   CHAIN       492    836       COAT PROTEIN VP1 (P1D).
FT   CHAIN       837    980       CORE PROTEIN P2A.
FT   CHAIN       981   1087       CORE PROTEIN P2B.
FT   CHAIN      1088   1422       CORE PROTEIN P2C.
FT   CHAIN      1423   1496       PROBABLE PROTEIN P3A.
FT   CHAIN      1497   1519       PROBABLE PROTEIN P3B.
FT   CHAIN      1520   1738       PROBABLE PROTEIN P3C.
FT   CHAIN      1739   2227       RNA-DIRECTED POLYMERASE 3D.
FT   VARIANT      77     77       K -> R (IN ATTENUATED STRAIN).
FT   VARIANT     764    764       E -> V (IN ATTENUATED STRAIN).
FT   VARIANT     821    821       N -> S (IN ATTENUATED STRAIN).
FT   VARIANT    1052   1052       A -> V (IN ATTENUATED STRAIN).
FT   VARIANT    1062   1062       G -> A (IN ATTENUATED STRAIN).
FT   VARIANT    1118   1118       K -> M (IN ATTENUATED STRAIN).
FT   VARIANT    1151   1151       E -> K (IN ATTENUATED STRAIN).
FT   VARIANT    1163   1163       F -> S (IN ATTENUATED STRAIN).
FT   VARIANT    1277   1277       V -> I (IN ATTENUATED STRAIN).
FT   VARIANT    1500   1500       H -> Y (IN ATTENUATED STRAIN).
FT   VARIANT    1805   1805       D -> N (IN ATTENUATED STRAIN).
FT   VARIANT    1930   1930       S -> T (IN ATTENUATED STRAIN).
SQ   SEQUENCE   2227 AA;  251506 MW;  01E225E7AEB740A6 CRC64;


  Query Match             100.0%;  Score 107;  DB 1;  Length 2227;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 SHIECRKPYKELRLEVGKQR 20
           ||||||||||||||||||||
Db     792 SHIECRKPYKELRLEVGKQR 811


RESULT   7
POLG_HPAVL
ID   POLG_HPAVL     STANDARD;      PRT;  2227 AA.
AC   P06441;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
DE   P2A TO P2C; PROBABLE PROTEINS P3A TO P3C; RNA-DIRECTED RNA POLYMERASE
DE   P3D (EC 2.7.7.48)].
OS   Hepatitis A virus (strain LA).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12099;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85190549; PubMed=2986127;
RA   Najarian R., Caput D., Gee W.W., Potter S.J., Renard A.,
RA   Merryweather J., van Nest G., Dina D.;
RT   "Primary structure and gene organization of human hepatitis A virus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:2627-2631(1985).
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K02990; AAA45472.1; -.
DR   PIR; A03903; GNNYHR.
DR   MEROPS; C03.005; -.
DR   InterPro; IPR000605; -.
DR   InterPro; IPR001205; -.
DR   Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR   Pfam; PF00910; RNA_helicase; 1.
KW   Polyprotein; Coat protein; Core protein; Transferase;
KW   RNA-directed RNA polymerase; Hydrolase; Thiol protease.
FT   CHAIN         1     23       COAT PROTEIN VP4 (P1A).
FT   CHAIN        24    245       COAT PROTEIN VP2 (P1B).
FT   CHAIN       246    491       COAT PROTEIN VP3 (P1C).
FT   CHAIN       492    836       COAT PROTEIN VP1 (P1D).
FT   CHAIN       837    980       CORE PROTEIN P2A.
FT   CHAIN       981   1076       CORE PROTEIN P2B.
FT   CHAIN      1077   1422       CORE PROTEIN P2C.
FT   CHAIN      1423   1484       PROBABLE PROTEIN P3A.
FT   CHAIN      1485   1507       PROBABLE PROTEIN P3B.
FT   CHAIN      1508   1678       PROBABLE PROTEIN P3C.
FT   CHAIN      1679   2227       RNA-DIRECTED POLYMERASE P3D.
SQ   SEQUENCE   2227 AA;  251898 MW;  99A7354B4CD2799C CRC64;


  Query Match             100.0%;  Score 107;  DB 1;  Length 2227;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 SHIECRKPYKELRLEVGKQR 20
           ||||||||||||||||||||
Db     792 SHIECRKPYKELRLEVGKQR 811


RESULT   8
POLG_HPAVM
ID   POLG_HPAVM     STANDARD;      PRT;  2227 AA.
AC   P13901; Q81083; Q81084; Q81085; Q81086; Q81087; Q81088; Q81089;
AC   Q81090; Q81091; Q81092; Q81093;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
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DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
DE   P2A TO P2C; PROBABLE PROTEINS P3A TO P3C; RNA-DIRECTED RNA POLYMERASE
DE   P3D (EC 2.7.7.48)].
OS   Hepatitis A virus (strain MBB).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12100;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88045071; PubMed=2823500;
RA   Paul A.V., Tada H., der Helm K., Wissel T., Kiehn R., Wimmer E.,
RA   Deinhardt F.;
RT   "The entire nucleotide sequence of the genome of human hepatitis A
RT   virus (isolate MBB).";
RL   Virus Res. 8:153-171(1987).
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- MISCELLANEOUS: THIS VIRUS WAS ISOLATED FROM THE STOOL OF A PATIENT
CC       WHO HAD BEEN INFECTED IN THE AFRICAN MEDITERRANEAN REGION.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M20273; AAA45474.1; -.
DR   PIR; JS0303; GNNYHB.
DR   MEROPS; C03.005; -.
DR   InterPro; IPR000605; -.
DR   InterPro; IPR001205; -.
DR   Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR   Pfam; PF00910; RNA_helicase; 1.
KW   Polyprotein; Coat protein; Core protein; Transferase;
KW   RNA-directed RNA polymerase; Hydrolase; Thiol protease.
FT   CHAIN         1     23       COAT PROTEIN VP4 (P1A).
FT   CHAIN        24    245       COAT PROTEIN VP2 (P1B).
FT   CHAIN       246    491       COAT PROTEIN VP3 (P1C).
FT   CHAIN       492    836       COAT PROTEIN VP1 (P1D).
FT   CHAIN       837    980       CORE PROTEIN P2A.
FT   CHAIN       981   1087       CORE PROTEIN P2B.
FT   CHAIN      1088   1422       CORE PROTEIN P2C.
FT   CHAIN      1423   1496       PROBABLE PROTEIN P3A.
FT   CHAIN      1497   1519       PROBABLE PROTEIN P3B.
FT   CHAIN      1520   1738       PROBABLE PROTEIN P3C.
FT   CHAIN      1739   2227       RNA-DIRECTED POLYMERASE 3D.
SQ   SEQUENCE   2227 AA;  251425 MW;  EC983ED2A7C86349 CRC64;


  Query Match             100.0%;  Score 107;  DB 1;  Length 2227;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db    792 SHIECRKPYKELRLEVGKQR 811


RESULT   9
POLG_HPAVG
ID   POLG_HPAVG     STANDARD;      PRT;   808 AA.
AC   Q02381;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEIN
DE   P2A] (FRAGMENT).
OS   Hepatitis A virus (strain GA76).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=31706;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92260183; PubMed=1316423;
RA   Khanna B., Spelbring J.E., Innis B.L., Robertson B.H.;
RT   "Characterization of a genetic variant of human hepatitis A virus.";
RL   J. Med. Virol. 36:118-124(1992).
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M66695; AAA45477.1; -.
KW   Polyprotein; Coat protein; Core protein.
FT   NON_TER       1      1
FT   CHAIN        <1      2       COAT PROTEIN VP4 (P1A).
FT   CHAIN         3    223       COAT PROTEIN VP2 (P1B).
FT   CHAIN       224    470       COAT PROTEIN VP3 (P1C).
FT   CHAIN       471    770       COAT PROTEIN VP1 (P1D).
FT   CHAIN       771   >808       CORE PROTEIN P2A.
FT   NON_TER     808    808
SQ   SEQUENCE   808 AA;  90632 MW;  D80CE7E57A479C12 CRC64;


  Query Match             88.8%;  Score 95;  DB 1;  Length 808;
  Best Local Similarity   95.0%;  Pred. No. 9e-08;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          |||| ||||||||||||||||
Db    771 SHIEKRKPYKELRLEVGKQR 790


RESULT  10
POLG_HPAVS
ID   POLG_HPAVS     STANDARD;      PRT;  2230 AA.
AC   P14553;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
DE   P2A TO P2C; PROBABLE PROTEINS P3A TO P3C; RNA-DIRECTED RNA POLYMERASE
DE   P3D (EC 2.7.7.48)].
OS   Simian hepatitis A virus (strain AGM-27).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12102;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91311420; PubMed=1649901;
RA   Tsarev S.A., Emerson S.U., Balayan M.S., Ticehurst J.R.,
RA   Purcell R.H.;
RT   "Simian hepatitis A virus (HAV) strain AGM-27: comparison of genome
RT   structure and growth in cell culture with other HAV strains.";
RL   J. Gen. Virol. 72:1677-1683(1991).
RN   [2]
RP   SEQUENCE OF 1750-2164 FROM N.A.
RX   MEDLINE=89232168; PubMed=2541023;
RA   Balayan M.S., Kusov Y.Y., Andjaparidze A.G., Tsarev S.A.,
RA   Sverdlov E.D., Chizhikov V.E., Blinov V.M., Vasilenko S.K.;
RT   "Variations in genome fragments coding for RNA polymerase in human
RT   and simian hepatitis A viruses.";
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RL   FEBS Lett. 247:425-428(1989).
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D00924; BAA00766.1; -.
DR   EMBL; X15461; CAA33490.1; -.
DR   PIR; A30470; GNNYSA.
DR   PIR; S04885; S04885.
DR   MEROPS; C03.005; -.
DR   InterPro; IPR000605; -.
DR   InterPro; IPR001205; -.
DR   Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR   Pfam; PF00910; RNA_helicase; 1.
KW   Polyprotein; Coat protein; Core protein; Transferase;
KW   RNA-directed RNA polymerase; Hydrolase; Thiol protease.
FT   CHAIN         1     27       COAT PROTEIN VP4 (P1A).
FT   CHAIN        28    249       COAT PROTEIN VP2 (P1B).
FT   CHAIN       250    495       COAT PROTEIN VP3 (P1C).
FT   CHAIN       496    795       COAT PROTEIN VP1 (P1D).
FT   CHAIN       796    984       CORE PROTEIN P2A.
FT   CHAIN       985   1091       CORE PROTEIN P2B.
FT   CHAIN      1092   1426       CORE PROTEIN P2C.
FT   CHAIN      1427   1498       PROBABLE PROTEIN 3A.
FT   CHAIN      1499   1521       PROBABLE PROTEIN 3B.
FT   CHAIN      1522   1741       PROBABLE PROTEIN 3C.
FT   CHAIN      1742   2230       RNA-DIRECTED POLYMERASE 3D.
SQ   SEQUENCE   2230 AA;  251296 MW;  87B3230E324E1F19 CRC64;


  Query Match             80.4%;  Score 86;  DB 1;  Length 2230;
  Best Local Similarity   85.0%;  Pred. No. 7.2e-06;
  Matches   17;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 SHIECRKPYKELRLEVGKQR 20
           ||||  |||||||:||||||
Db     796 SHIEQGKPYKELRMEVGKQR 815


RESULT  11
POLG_HPAVT
ID   POLG_HPAVT     STANDARD;      PRT;   839 AA.
AC   P31788;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEIN
DE   P2A] (FRAGMENT).
OS   Simian hepatitis A virus (strain CY-145).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=31707;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91311421; PubMed=1649902;
RA   Nainan O.V., Margolis H.S., Robertson B.H., Balayan M., Brinton M.A.;
RT   "Sequence analysis of a new hepatitis A virus naturally infecting
RT   cynomolgus macaques (Macaca fascicularis).";
RL   J. Gen. Virol. 72:1685-1689(1991).
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M59286; AAA45473.1; -.
DR   PIR; JQ1180; GNNYS2.
KW   Polyprotein; Coat protein; Core protein.
FT   CHAIN         1     23       COAT PROTEIN VP4 (P1A).
FT   CHAIN        24    245       COAT PROTEIN VP2 (P1B).
FT   CHAIN       246    491       COAT PROTEIN VP3 (P1C).
FT   CHAIN       492      ?       COAT PROTEIN VP1 (P1D).
FT   CHAIN         ?   >839       CORE PROTEIN P2A.
FT   NON_TER     839    839
SQ   SEQUENCE   839 AA;  93825 MW;  2CACC4BD1E192DBC CRC64;


  Query Match             79.0%;  Score 84.5;  DB 1;  Length 839;
  Best Local Similarity   90.0%;  Pred. No. 4.7e-06;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    1;  Gaps    1;

Qy       1 SHIECRKPYKELRLEVGKQR 20
           |||| :|||||||||||||||
Db     792 SHIE-KKPYKELRLEVGKQR 810


RESULT  12
YAGA_SCHPO
ID   YAGA_SCHPO     STANDARD;      PRT;   420 AA.
AC   Q09873;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   01-FEB-1996 (Rel. 33, Last annotation update)
DE   HYPOTHETICAL 47.5 KDA PROTEIN C12G12.10 IN CHROMOSOME I.
GN   SPAC12G12.10.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   Devlin K., Odell C., Churcher C.M., Barrell B.G., Rajandream M.A.,
RA   Walsh S.V.;
RL   Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z66568; CAA91505.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   420 AA;  47525 MW;  9DC1F710FBEB9761 CRC64;


  Query Match             43.0%;  Score 46;  DB 1;  Length 420;
  Best Local Similarity   46.7%;  Pred. No. 4.2;
  Matches    7;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4 ECRKPYKELRLEVGK 18
           :|  |:||:|:: ||
Db     376 DCSLPFKEMRVDDGK 390
```

```
RESULT  13
CO3_RAT
ID   CO3_RAT        STANDARD;      PRT;  1663 AA.
AC   P01026;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   01-FEB-1996 (Rel. 33, Last annotation update)
DE   COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN].
GN   C3.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR; TISSUE=Liver;
RX   MEDLINE=90245672; PubMed=2336397;
RA   Misumi Y., Sohda M., Ikehara Y.;
RT   "Nucleotide and deduced amino acid sequence of rat complement C3.";
RL   Nucleic Acids Res. 18:2178-2178(1990).
RN   [2]
RP   SEQUENCE OF 671-748.
RX   MEDLINE=79062262; PubMed=309768;
RA   Jacobs J.W., Rubin J.S., Hugli T.E., Bogardt R.A., Mariz I.K.,
RA   Daniels J.S., Daughaday W.H., Bradshaw R.A.;
RT   "Purification, characterization, and amino acid sequence of rat
RT   anaphylatoxin (C3a).";
RL   Biochemistry 17:5031-5038(1978).
RN   [3]
RP   SEQUENCE OF 1316-1595 FROM N.A.
RX   MEDLINE=89380332; PubMed=2674144;
RA   Sundstrom S.A., Komm B.S., Ponce-De-Leon H., Yi Z., Teuscher C.,
RA   Lyttle C.R.;
RT   "Estrogen regulation of tissue-specific expression of complement C3.";
RL   J. Biol. Chem. 264:16941-16947(1989).
CC   -!- FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE
CC       COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL
CC       REACTION IN BOTH CLASSICAL AND ALTERNATIVE COMPLEMENT PATHWAYS.
CC       AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE
CC       THIOLESTER, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES.
CC   -!- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C3,
CC       C3A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
CC       INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
CC       PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
CC       BASOPHILIC LEUKOCYTES.
CC   -!- SUBUNIT: C3 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 ARG
CC       RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE
CC       BOND. C3 CONVERTASE ACTIVATES C3 BY CLEAVING THE ALPHA CHAIN,
CC       RELEASING C3A ANAPHYLATOXIN & GENERATING C3B (BETA CHAIN + ALPHA'
CC       CHAIN).
CC   -!- SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN.
CC   -!- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X52477; CAA36716.1; -.
DR   EMBL; M29866; AAA40837.1; ALT_SEQ.
DR   PIR; A01260; A01260.
DR   PIR; S15764; S15764.
DR   HSSP; P01024; 1C3D.
DR   InterPro; IPR000020; -.
DR   InterPro; IPR001134; -.
DR   InterPro; IPR001599; -.
DR   InterPro; IPR001840; -.
DR   InterPro; IPR002890; -.
DR   Pfam; PF00207; A2M; 1.
DR   Pfam; PF01835; A2M_N; 1.
DR   Pfam; PF01821; ANATO; 1.
DR   Pfam; PF01759; NTR; 1.
DR   PRINTS; PR00004; ANAPHYLATOXN.
DR   PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR   PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR   PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
KW   Complement pathway; Complement alternate pathway; Plasma;
KW   Inflammatory response; Glycoprotein; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25   1663       COMPLEMENT C3.
FT   CHAIN        25    666       BETA CHAIN.
FT   CHAIN       671   1663       ALPHA CHAIN.
FT   PEPTIDE     671    748       C3A ANAPHYLATOXIN.
FT   CHAIN       749   1663       C3B (ALPHA' CHAIN).
FT   SITE        748    749       CLEAVAGE (BY C3 CONVERTASE).
FT   DOMAIN      693    728       ANAPHYLATOXIN-LIKE.
FT   DISULFID    558    816       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    626    661       BY SIMILARITY.
FT   DISULFID    693    720       BY SIMILARITY.
FT   DISULFID    694    727       BY SIMILARITY.
FT   DISULFID    707    728       BY SIMILARITY.
FT   DISULFID    873   1513       BY SIMILARITY.
FT   DISULFID   1101   1158       BY SIMILARITY.
FT   DISULFID   1358   1489       BY SIMILARITY.
FT   DISULFID   1389   1458       BY SIMILARITY.
FT   DISULFID   1506   1511       BY SIMILARITY.
FT   DISULFID   1518   1590       BY SIMILARITY.
FT   DISULFID   1537   1661       BY SIMILARITY.
FT   THIOLEST   1010   1013
FT   CARBOHYD    939    939       N-LINKED (GLCNAC. . .) (PROBABLE).
FT   CARBOHYD   1617   1617       N-LINKED (GLCNAC. . .) (PROBABLE).
FT   CONFLICT    721    722       LK -> KL (IN REF. 2).
SQ   SEQUENCE   1663 AA;  186460 MW;  2F87CCB143CDD4BC CRC64;


  Query Match             40.7%;  Score 43.5;  DB 1;  Length 1663;
  Best Local Similarity   47.4%;  Pred. No. 42;
  Matches    9;  Conservative    4;  Mismatches    3;  Indels    3;  Gaps    1;

Qy       1 SHIECRKPYKELRLEVGKQ 19
           ||::||     |:|: |||
Db    1586 SHVKCR---NALKLQKGKQ 1601


RESULT  14
NCAP_HRSV1
ID   NCAP_HRSV1     STANDARD;      PRT;   391 AA.
AC   P24566;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   01-MAR-1992 (Rel. 21, Last annotation update)
DE   NUCLEOCAPSID PROTEIN.
GN   N.
OS   Human respiratory syncytial virus (subgroup B / strain 18537).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX   NCBI_TaxID=11251;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89279331; PubMed=2525176;
RA   Johnson P.R., Collins P.L.;
RT   "The 1B (NS2), 1C (NS1) and N proteins of human respiratory syncytial
RT   virus (RSV) of antigenic subgroups A and B: sequence conservation and
RT   divergence within RSV genomic RNA.";
RL   J. Gen. Virol. 70:1539-1547(1989).
CC   -!- FUNCTION: MOST ABUNDANT PROTEIN IN THE VIRION AND AN IMPORTANT
CC       ELEMENT CONFERRING HELICAL SYMMETRY ON THE NUCLEOPROTEIN CORE AS
CC       WELL AS INTERACTING WITH M PROTEIN DURING VIRION FORMATION.
CC   -!- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES NUCLEOCAPSID FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; D00736; BAA00637.1; -.
DR   PIR; C32063; VHNZ3.
KW   Nucleocapsid.
SQ   SEQUENCE   391 AA;  43416 MW;  9A2BBB50103B2835 CRC64;


  Query Match             40.2%;  Score 43;  DB 1;  Length 391;
  Best Local Similarity   56.2%;  Pred. No. 12;
  Matches    9;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3 IECRKPYKELRLEVGK 18
           || || ||:|  |:|:
Db     129 IESRKSYKKLLKEMGE 144


RESULT  15
LOLA_XYLFA
ID   LOLA_XYLFA     STANDARD;      PRT;   210 AA.
AC   Q9PDC7;
DT   01-OCT-2000 (Rel. 40, Created)
DT   01-OCT-2000 (Rel. 40, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   OUTER-MEMBRANE LIPOPROTEINS CARRIER PROTEIN PRECURSOR.
GN   LOLA OR XF1452.
OS   Xylella fastidiosa.
OC   Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC   Xylella.
OX   NCBI_TaxID=2371;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=9A5C;
RX   MEDLINE=20365717; PubMed=10910347;
RA   Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA   Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA   Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA   Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA   Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA   Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA   Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA   Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA   Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA   Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA   Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA   Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA   Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA   Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA   Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA   Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA   Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA   de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA   Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA   Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA   de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA   da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA   da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA   de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA   Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA   Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT   "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL   Nature 406:151-159(2000).
CC   -!- FUNCTION: PARTICIPATES IN THE TRANSLOCATION OF LIPOPROTEINS FROM
CC       THE INNER MEMBRANE TO THE OUTER MEMBRANE. ONLY FORMS A COMPLEX
CC       WITH A LIPOPROTEIN IF THE RESIDUE AFTER THE N-TERMINAL CYS IS NOT
CC       AN ASPARTATE (THE ASP ACTS AS A TARGETING SIGNAL TO INDICATE THAT
CC       THE LIPOPROTEIN SHOULD STAY IN THE INNER MEMBRANE) (BY
CC       SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: PERIPLASMIC (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LOLA FAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; AE003975; AAF84261.1; ALT_INIT.
KW   Chaperone; Transport; Protein transport; Periplasmic; Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    210       OUTER-MEMBRANE LIPOPROTEINS CARRIER
FT                                PROTEIN.
SQ   SEQUENCE   210 AA;  23618 MW;  08EB8BA44005B24F CRC64;


  Query Match             39.3%;  Score 42;  DB 1;  Length 210;
  Best Local Similarity   50.0%;  Pred. No. 9.3;
  Matches    8;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       4 ECRKPYKELRLEVGKQ 19
           ||  |||:| :  ||:
Db      73 ECDAPYKQLVVADGKR 88


Search completed: April 24, 2001, 16:33:53
Job time: 549 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2001, 16:21:06 ; Search time 73.14 Seconds
(without alignments)
18.792 Million cell updates/sec

Title: US-09-171-432A-39
Perfect score: 107
Sequence: 1 SHIECRKPYKELRLEVGKQR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_67:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	107	100.0	56	2	PQ0431	genome polyprotein
2	107	100.0	341	2	S04137	genome polyprotein
3	107	100.0	852	1	GNNYHA	genome polyprotein
4	107	100.0	1358	2	A03905	genome polyprotein
5	107	100.0	2227	1	GNNYHM	genome polyprotein
6	107	100.0	2227	1	GNNYHR	genome polyprotein
7	107	100.0	2227	1	GNNYMK	genome polyprotein
8	107	100.0	2227	1	GNNYHB	genome polyprotein
9	105	98.1	56	2	PQ0427	genome polyprotein
10	104	97.2	56	2	PQ0429	genome polyprotein
11	102	95.3	319	2	JH0135	genome polyprotein
12	100	93.5	56	2	PQ0430	genome polyprotein
13	97	90.7	56	2	PQ0432	genome polyprotein
14	96	89.7	56	2	PQ0428	genome polyprotein
15	95	88.8	56	2	PQ0434	genome polyprotein
16	87	81.3	55	2	PQ0433	genome polyprotein
17	86	80.4	56	2	PQ0436	genome polyprotein
18	86	80.4	2230	1	GNNYSA	genome polyprotein
19	84.5	79.0	55	2	PQ0435	genome polyprotein
20	84.5	79.0	839	1	GNNYS2	genome polyprotein
21	81	75.7	56	2	PQ0437	genome polyprotein
22	46	43.0	420	2	S62541	hypothetical prote
23	44	41.1	374	2	C84040	hypothetical prote
24	43.5	40.7	1663	1	C3RT	complement C3 prec
25	43	40.2	339	2	T18926	hypothetical prote
26	43	40.2	346	2	T27896	hypothetical prote
27	43	40.2	391	1	VHNZ3	nucleocapsid prote
28	43	40.2	554	2	T49917	hypothetical prote
29	42.5	39.7	140	2	E64364	hypothetical prote
30	42	39.3	121	2	T17708	hypothetical prote
31	42	39.3	214	2	E82679	chaperone XF1452 [
32	42	39.3	286	2	S07532	puff II/9-1 protei
33	42	39.3	329	2	T25067	hypothetical prote
34	42	39.3	494	2	S62902	legumin 2 precurso
35	42	39.3	723	2	D71091	methionine--tRNA l
36	42	39.3	1087	2	T16876	hypothetical prote
37	42	39.3	1157	2	T43259	pyruvate (flavodox
38	42	39.3	1270	2	T22615	hypothetical prote
39	41	38.3	298	2	B83823	endonuclease IV BH
40	41	38.3	364	2	C64326	succinyl-CoA synth
41	41	38.3	370	2	H64480	hypothetical prote
42	41	38.3	391	1	VHNZ1	nucleocapsid prote
43	41	38.3	391	1	VHNZB4	nucleocapsid prote
44	41	38.3	391	1	JQ1533	nucleocapsid prote
45	41	38.3	467	1	VHNZ	nucleocapsid prote

ALIGNMENTS

RESULT 1
PQ0431
genome polyprotein - human hepatitis A virus (strain No. 4) (fragment)
C;Species: human hepatitis A virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PQ0431
R;Robertson, B.H.; Jansen, R.W.; Khanna, B.; Totsuka, A.; Nainan, O.V.; Siegl, G.; Wi
J. Gen. Virol. 73, 1365-1377, 1992
A;Title: Genetic relatedness of hepatitis A virus strains recovered from different ge
A;Reference number: PQ0427; MUID:92300330
A;Accession: PQ0431
A;Molecule type: mRNA
A;Residues: 1-56 <ROB>
A;Note: this protein is from the VP1/2A Junction region
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; polyprotein

Query Match 100.0%; Score 107; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 SHIECRKPYKELRLEVGKQR 20
           ||||||||||||||||||||
Db      29 SHIECRKPYKELRLEVGKQR 48
```

RESULT 2
S04137
genome polyprotein - human hepatitis A virus (strain LCDC-1) (fragment)
C;Species: human hepatitis A virus
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 21-Jul-2000
C;Accession: S04137
R;Andonov, A.P.; Lau, P.C.K.; Chaudhary, R.
Nucleic Acids Res. 17, 3594, 1989
A;Title: Nucleotide sequence of the VP1 gene from a Chinese strain of hepatitis A vir
A;Reference number: S04137; MUID:89263805
A;Accession: S04137
A;Molecule type: mRNA
A;Residues: 1-341 <AND>
A;Cross-references: EMBL:X14666; NID:g62301; PIDN:CAA32794.1; PID:g4377576
C;Genetics:
A;Gene: VP1
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; polyprotein
F;2-340/Product: coat protein 1D (VP1) #status predicted <MAT>

Query Match 100.0%; Score 107; DB 2; Length 341;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db    296 SHIECRKPYKELRLEVGKQR 315
```

RESULT 3
GNNYHA
genome polyprotein - human hepatitis A virus (strain CR326) (fragment)
N;Contains: coat protein 1A; coat protein 1B; coat protein 1C; core protein 2A
C;Species: human hepatitis A virus
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
C;Accession: A03904
R;Linemeyer, D.L.; Menke, J.G.; Martin-Gallardo, A.; Hughes, J.V.; Young, A.; Mitra, S.W
J. Virol. 54, 247-255, 1985
A;Title: Molecular cloning and partial sequencing of hepatitis A viral cDNA.
A;Reference number: A03904; MUID:85185648
A;Accession: A03904
A;Molecule type: genomic RNA
A;Residues: 1-852 <LIN>
A;Cross-references: EMBL:M10033; NID:g329592; PIDN:AAA45470.1; PID:g329593
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; polyprotein
F;1-245/Product: coat protein 1A #status predicted <C1A>
F;246-491/Product: coat protein 1B #status predicted <C1B>
F;492-836/Product: coat protein 1C #status predicted <C1C>
F;837-852/Product: core protein 2A (fragment) #status predicted <C2A>

Query Match 100.0%; Score 107; DB 1; Length 852;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db    792 SHIECRKPYKELRLEVGKQR 811
```

RESULT 4
A03905
genome polyprotein (version 2) - human hepatitis A virus (fragments)
N;Contains: coat protein 1A; coat protein 1B; coat protein 1C; core protein 2A; protein
C;Species: human hepatitis A virus
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 15-Nov-1996
C;Accession: A03905
R;Baroudy, B.M.; Ticehurst, J.R.; Miele, T.A.; Maizel Jr., J.V.; Purcell, R.H.; Feinstor
Proc. Natl. Acad. Sci. U.S.A. 82, 2143-2147, 1985
A;Title: Sequence analysis of hepatitis A virus cDNA coding for capsid proteins and RNA
A;Reference number: A03905; MUID:85166289
A;Accession: A03905
A;Molecule type: genomic RNA
A;Residues: 1-1358 <BAR>
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; polyprotein
F;1-245/Product: coat protein 1A #status predicted <C1A>
F;246-491/Product: coat protein 1B #status predicted <C1B>
F;492-836/Product: coat protein 1C #status predicted <C1C>
F;837-854/Product: core protein 2A (fragment) #status predicted <C2A>
F;855-1358/Product: protein 3D (RNA polymerase) (fragment) #status predicted <C3D>

Query Match 100.0%; Score 107; DB 2; Length 1358;
Best Local Similarity 100.0%; Pred. No. 6.8e-09;
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Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db    792 SHIECRKPYKELRLEVGKQR 811
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RESULT 5
GNNYHM
genome polyprotein - human hepatitis A virus (strain HM-175, wild type)
N;Contains: coat protein 1A; coat protein 1B; coat protein 1C; coat protein 1D; core
B; RNA-directed RNA polymerase (EC 2.7.7.48), protein 3D
C;Species: human hepatitis A virus
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jul-1999
C;Accession: A25981
R;Cohen, J.I.; Ticehurst, J.R.; Purcell, R.H.; Buckler-White, A.; Baroudy, B.M.
J. Virol. 61, 50-59, 1987
A;Title: Complete nucleotide sequence of wild-type hepatitis A virus: comparison with
A;Reference number: A25981; MUID:87061253
A;Accession: A25981
A;Molecule type: genomic RNA
A;Residues: 1-2227 <COH>
A;Cross-references: EMBL:M14707; NID:g329582; PIDN:AAA45465.1; PID:g329583
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; cysteine proteinase; hydrolase; nucleotidyltr
F;1-23/Product: coat protein 1A #status predicted <VP4>
F;24-245/Product: coat protein 1B #status predicted <VP2>
F;246-491/Product: coat protein 1C #status predicted <VP3>
F;492-791/Product: coat protein 1D #status predicted <VP1>
F;792-980/Product: core protein 2A #status predicted <C2A>
F;981-1087/Product: core protein 2B #status predicted <C2B>
F;1088-1422/Product: core protein 2C #status predicted <C2C>
F;1423-1496/Product: protein 3A #status predicted <C3A>
F;1497-1519/Product: protein 3B #status predicted <C3B>
F;1520-1738/Product: cysteine proteinase, protein 3C #status predicted <C3C>
F;1739-2227/Product: RNA-directed RNA polymerase, protein 3D #status predicted <C3D>

Query Match 100.0%; Score 107; DB 1; Length 2227;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
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Qy      1 SHIECRKPYKELRLEVGKQR 20
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Db    792 SHIECRKPYKELRLEVGKQR 811
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RESULT 6
GNNYHR
genome polyprotein - human hepatitis A virus
N;Contains: coat protein 1A; coat protein 1B; coat protein 1C; core protein 2A; core
NA polymerase (EC 2.7.7.48), protein 3D
C;Species: human hepatitis A virus
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
C;Accession: A03903
R;Najarian, R.; Caput, D.; Gee, W.; Potter, S.J.; Renard, A.; Merryweather, J.; van N
Proc. Natl. Acad. Sci. U.S.A. 82, 2627-2631, 1985
A;Title: Primary structure and gene organization of human hepatitis A virus.
A;Reference number: A03903; MUID:85190549
A;Accession: A03903
A;Molecule type: genomic RNA
A;Residues: 1-2227 <NAJ>
A;Cross-references: GB:K02990; NID:g329596; PIDN:AAA45472.1; PID:g329597
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; cysteine proteinase; hydrolase; nucleotidyltr
F;1-245/Product: coat protein 1A #status predicted <C1A>
F;246-491/Product: coat protein 1B #status predicted <C1B>
F;492-836/Product: coat protein 1C #status predicted <C1C>
F;837-980/Product: core protein 2A #status predicted <C2A>
F;981-1076/Product: core protein 2B #status predicted <C2B>
F;1077-1422/Product: core protein 2C #status predicted <C2C>
F;1423-1484/Product: protein 3A #status predicted <C3A>
F;1485-1507/Product: protein 3B #status predicted <C3B>
F;1508-1678/Product: cysteine proteinase, protein 3C #status predicted <C3C>
F;1679-2227/Product: RNA-directed RNA polymerase, protein 3D #status predicted <C3D>

Query Match 100.0%; Score 107; DB 1; Length 2227;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SHIECRKPYKELRLEVGKQR 20
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Db    792 SHIECRKPYKELRLEVGKQR 811


RESULT   7
GNNYMK
genome polyprotein - human hepatitis A virus (strain HM-175/7MK-5, attenuated HAV)
N;Contains: coat protein 1A; coat protein 1B; coat protein 1C; core protein 2A; core pro
NA polymerase (EC 2.7.7.48), protein 3D
C;Species: human hepatitis A virus
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
C;Accession: A94149; A25914; A94508
R;Cohen, J.I.; Rosenblum, B.; Ticehurst, J.R.; Daemer, R.J.; Feinstone, S.M.; Purcell, R
Proc. Natl. Acad. Sci. U.S.A. 84, 2497-2501, 1987
A;Title: Complete nucleotide sequence of an attenuated hepatitis A virus: comparison wit
A;Reference number: A94149; MUID:87175701
A;Accession: A94149
A;Status: nucleic acid sequence not shown
A;Molecule type: genomic RNA
A;Residues: 1-2227 <COH>
A;Cross-references: EMBL:M16632; NID:g329594; PIDN:AAA45471.1; PID:g329595
A;Note: submitted to GenBank, August 1987
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; cysteine proteinase; hydrolase; nucleotidyltrans
F;1-245/Product: coat protein 1A #status predicted <P1A>
F;246-491/Product: coat protein 1B #status predicted <P1B>
F;492-836/Product: coat protein 1C #status predicted <P1C>
F;837-980/Product: core protein 2A #status predicted <P2A>
F;981-1076/Product: core protein 2B #status predicted <P2B>
F;1077-1422/Product: core protein 2C #status predicted <P2C>
F;1423-1484/Product: protein 3A #status predicted <P3A>
F;1485-1507/Product: protein 3B #status predicted <P3B>
F;1508-1678/Product: cysteine proteinase, protein 3C #status predicted <P3C>
F;1679-2227/Product: RNA-directed RNA polymerase, protein 3D #status predicted <P3D>


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Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db    792 SHIECRKPYKELRLEVGKQR 811


RESULT   8
GNNYHB
genome polyprotein - human hepatitis A virus (strain MBB)
N;Contains: coat protein 1A; coat protein 1B; coat protein 1C; coat protein 1D; core pro
 VPg; protein 3A; RNA-directed RNA polymerase (EC 2.7.7.48), protein 3D
C;Species: human hepatitis A virus
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-May-1996
C;Accession: JS0303
R;Paul, A.V.; Tada, H.; von der Helm, K.; Wissel, T.; Kiehn, R.; Wimmer, E.; Deinhardt,
Virus Res. 8, 153-171, 1987
A;Title: The entire nucleotide sequence of the genome of human hepatitis A virus (isolat
A;Reference number: JS0303; MUID:88045071
A;Accession: JS0303
A;Molecule type: genomic RNA
A;Residues: 1-2227 <PAU>
A;Cross-references: EMBL:M20273
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; cysteine proteinase; genome-linked protein; hydr
F;1-23/Product: coat protein 1A #status predicted <VP4>
F;24-246/Product: coat protein 1B #status predicted <VP2>
F;247-491/Product: coat protein 1C #status predicted <VP3>
F;492-836/Product: coat protein 1D #status predicted <VP1>
F;837-980/Product: core protein 2A #status predicted <P2A>
F;981-1108/Product: core protein 2B #status predicted <P2B>
F;1109-1438/Product: core protein 2C #status predicted <P2C>
F;1439-1496/Product: protein 3A #status predicted <P3A>
F;1497-1519/Product: genome-linked protein VPg #status predicted <VPG>
F;1520-1736/Product: cysteine proteinase, protein 3C #status predicted <P3C>
F;1737-2227/Product: RNA-directed RNA polymerase, protein 3D #status predicted <P3D>


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Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db    792 SHIECRKPYKELRLEVGKQR 811


RESULT   9
PQ0427
genome polyprotein - human hepatitis A virus (strain EP-35.730) (fragment)
C;Species: human hepatitis A virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PQ0427
R;Robertson, B.H.; Jansen, R.W.; Khanna, B.; Totsuka, A.; Nainan, O.V.; Siegl, G.; Wi
J. Gen. Virol. 73, 1365-1377, 1992
A;Title: Genetic relatedness of hepatitis A virus strains recovered from different ge
A;Reference number: PQ0427; MUID:92300330
A;Accession: PQ0427
A;Molecule type: mRNA
A;Residues: 1-56 <ROB>
C;Comment: This protein is from the VP1/2A Junction region.
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; polyprotein


  Query Match             98.1%;  Score 105;  DB 2;  Length 56;
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Qy      1 SHIECRKPYKELRLEVGKQR 20
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Db     29 SHIECRKPYKELRMEVGKQR 48


RESULT  10
PQ0429
genome polyprotein - human hepatitis A virus (strain PRC16) (fragment)
C;Species: human hepatitis A virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PQ0429
R;Robertson, B.H.; Jansen, R.W.; Khanna, B.; Totsuka, A.; Nainan, O.V.; Siegl, G.; Wi
J. Gen. Virol. 73, 1365-1377, 1992
A;Title: Genetic relatedness of hepatitis A virus strains recovered from different ge
A;Reference number: PQ0427; MUID:92300330
A;Accession: PQ0429
A;Molecule type: mRNA
A;Residues: 1-56 <ROB>
A;Note: this protein is from the VP1/2A Junction region
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; polyprotein


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Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||:||||||||||
Db     29 SHIECRKPYKDLRLEVGKQR 48


RESULT  11
JH0135
genome polyprotein - human hepatitis A virus (strain MS-1) (fragment)
N;Contains: amino end of core protein 2A; coat protein 1D
```

```
C;Species: human hepatitis A virus
A;Note: host Homo sapiens (man)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 08-Apr-1994
C;Accession: JH0135
R;Robertson, B.H.; Brown, V.K.; Bradley, D.W.
Virus Res. 8, 309-316, 1987
A;Title: Nucleic acid sequence of the VP1 region of attenuated MS-1 hepatitis A virus.
A;Reference number: JH0135; MUID:88129044
A;Accession: JH0135
A;Molecule type: genomic RNA
A;Residues: 1-319 <ROB>
A;Cross-references: GB:M22821
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; glycoprotein; polyprotein
F;1-300/Product: coat protein 1D #status predicted <CPD>
F;301-319/Product: core protein 2A (fragment) #status predicted <C2A>
F;237/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             95.3%;  Score 102;  DB 2;  Length 319;
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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 SHIECRKPYKELRLEVGKQ 19
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Db     301 SHIECRKPYKELRLEVGKQ 319


RESULT  12
PQ0430
genome polyprotein - human hepatitis A virus (strain S23-1) (fragment)
C;Species: human hepatitis A virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PQ0430
R;Robertson, B.H.; Jansen, R.W.; Khanna, B.; Totsuka, A.; Nainan, O.V.; Siegl, G.; Widel
J. Gen. Virol. 73, 1365-1377, 1992
A;Title: Genetic relatedness of hepatitis A virus strains recovered from different geogr
A;Reference number: PQ0427; MUID:92300330
A;Accession: PQ0430
A;Molecule type: mRNA
A;Residues: 1-56 <ROB>
A;Note: this protein is from the VP1/2A Junction region
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; polyprotein


  Query Match             93.5%;  Score 100;  DB 2;  Length 56;
  Best Local Similarity   95.0%;  Pred. No. 3.5e-09;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 SHIECRKPYKELRLEVGKQR 20
           ||||| |||||||||||||||
Db      29 SHIECGKPYKELRLEVGKQR 48


RESULT  13
PQ0432
genome polyprotein - human hepatitis A virus (strain CF-53) (fragment)
C;Species: human hepatitis A virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PQ0432
R;Robertson, B.H.; Jansen, R.W.; Khanna, B.; Totsuka, A.; Nainan, O.V.; Siegl, G.; Widel
J. Gen. Virol. 73, 1365-1377, 1992
A;Title: Genetic relatedness of hepatitis A virus strains recovered from different geogr
A;Reference number: PQ0427; MUID:92300330
A;Accession: PQ0432
A;Molecule type: mRNA
A;Residues: 1-56 <ROB>
A;Note: this protein is from the VP1/2A Junction region
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; polyprotein


  Query Match             90.7%;  Score 97;  DB 2;  Length 56;
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  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 SHIECRKPYKELRLEVGKQR 20
           |||| |||||||||||||||
Db      29 SHIESRKPYKELRLEVGKQR 48


RESULT  14
PQ0428
genome polyprotein - human hepatitis A virus (strain TKM002) (fragment)
C;Species: human hepatitis A virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PQ0428
R;Robertson, B.H.; Jansen, R.W.; Khanna, B.; Totsuka, A.; Nainan, O.V.; Siegl, G.; Wi
J. Gen. Virol. 73, 1365-1377, 1992
A;Title: Genetic relatedness of hepatitis A virus strains recovered from different ge
A;Reference number: PQ0427; MUID:92300330
A;Accession: PQ0428
A;Molecule type: mRNA
A;Residues: 1-56 <ROB>
A;Note: this protein is from the VP1/2A Junction region
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; polyprotein


  Query Match             89.7%;  Score 96;  DB 2;  Length 56;
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  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 SHIECRKPYKELRLEVGKQR 20
           |||| |||||||||||||||
Db      29 SHIEYRKPYKELRLEVGKQR 48


RESULT  15
PQ0434
genome polyprotein - human hepatitis A virus (strain KPH) (fragment)
C;Species: human hepatitis A virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PQ0434
R;Robertson, B.H.; Jansen, R.W.; Khanna, B.; Totsuka, A.; Nainan, O.V.; Siegl, G.; Wi
J. Gen. Virol. 73, 1365-1377, 1992
A;Title: Genetic relatedness of hepatitis A virus strains recovered from different ge
A;Reference number: PQ0427; MUID:92300330
A;Accession: PQ0434
A;Molecule type: mRNA
A;Residues: 1-56 <ROB>
A;Note: this protein is from the VP1/2A Junction region
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; polyprotein


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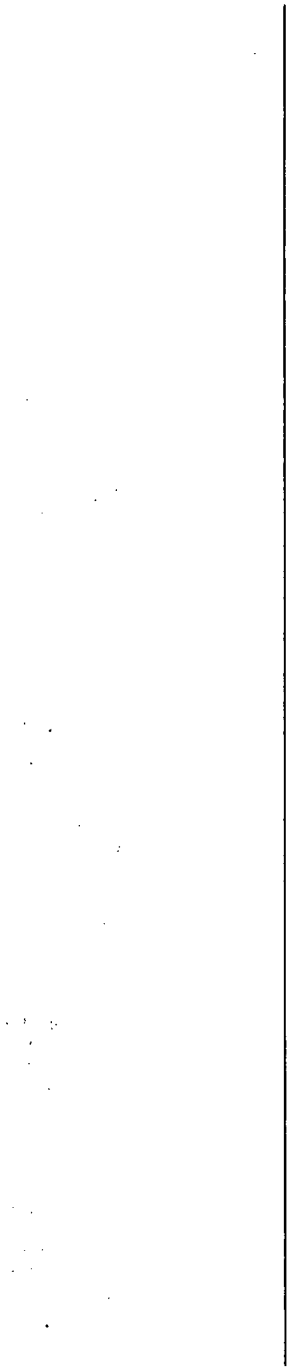

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2001, 16:26:09 ; Search time 62.1 Seconds
(without alignments)
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Title: US-09-171-432A-39
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Sequence: 1 SHIECRKPYKELRLEVGKQR 20

Scoring table: BLOSUM62
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Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	107	100.0	1091	6	5516630-2	Patent No. 5516630
2	107	100.0	2227	4	US-08-475-886-2	Sequence 2, Appli
3	107	100.0	2227	4	US-08-475-886-4	Sequence 4, Appli
4	107	100.0	2227	4	US-08-475-886-6	Sequence 6, Appli
5	107	100.0	2227	4	US-08-397-232-2	Sequence 2, Appli
6	107	100.0	2227	4	US-08-397-232-4	Sequence 4, Appli
7	84.5	79.0	839	1	US-08-087-016-2	Sequence 2, Appli
8	43	40.2	1127	4	US-09-150-460B-11	Sequence 11, Appl
9	41	38.3	391	5	PCT-US91-08177-3	Sequence 3, Appli
10	41	38.3	4544	1	US-08-469-486-52	Sequence 52, Appl
11	41	38.3	4544	2	US-08-469-658-52	Sequence 52, Appl
12	39	36.4	24	1	US-08-406-347A-13	Sequence 13, Appl
13	39	36.4	344	4	US-09-393-554-2	Sequence 2, Appli
14	39	36.4	520	6	5223391-5	Patent No. 5223391
15	39	36.4	1235	2	US-08-680-326-36	Sequence 36, Appl
16	38	35.5	31	1	US-08-015-770B-26	Sequence 26, Appl
17	38	35.5	31	1	US-08-488-252-15	Sequence 15, Appl
18	38	35.5	102	2	US-08-651-940-3	Sequence 3, Appli
19	38	35.5	155	2	US-08-651-940-4	Sequence 4, Appli
20	38	35.5	256	2	US-08-719-758-2	Sequence 2, Appli
21	38	35.5	256	4	US-09-119-827-2	Sequence 2, Appli
22	38	35.5	364	2	US-08-651-940-2	Sequence 2, Appli
23	38	35.5	364	4	US-09-025-580-37	Sequence 37, Appl
24	38	35.5	372	4	US-09-286-904-24	Sequence 24, Appl
25	37.5	35.0	309	4	US-09-166-412-2	Sequence 2, Appli
26	37	34.6	67	6	5196333-10	Patent No. 5196333
27	37	34.6	68	1	US-08-606-789-8	Sequence 8, Appli
28	37	34.6	68	2	US-09-111-348-8	Sequence 8, Appli
29	37	34.6	69	5	PCT-US95-06406A-6	Sequence 6, Appli
30	37	34.6	469	2	US-08-968-751-2	Sequence 2, Appli
31	37	34.6	493	6	5196333-4	Patent No. 5196333
32	37	34.6	855	2	US-08-468-558-2	Sequence 2, Appli
33	37	34.6	972	3	US-08-335-844A-24	Sequence 24, Appl
34	36.5	34.1	188	2	US-08-933-750C-8	Sequence 8, Appli
35	36.5	34.1	188	4	US-09-234-613-8	Sequence 8, Appli
36	36.5	34.1	609	2	US-08-716-301-4	Sequence 4, Appli
37	36	33.6	102	3	US-08-906-769-125	Sequence 125, App
38	36	33.6	102	4	US-08-906-616-125	Sequence 125, App
39	36	33.6	102	4	US-08-639-075A-125	Sequence 125, App
40	36	33.6	102	4	US-09-012-431-125	Sequence 125, App
41	36	33.6	183	1	US-07-841-646-23	Sequence 23, Appl
42	36	33.6	183	1	US-08-147-023-23	Sequence 23, Appl
43	36	33.6	183	1	US-08-447-570-23	Sequence 23, Appl
44	36	33.6	183	2	US-08-449-700-23	Sequence 23, Appl
45	36	33.6	183	2	US-08-449-699A-23	Sequence 23, Appl

ALIGNMENTS

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;Patent No. 5516630
;     APPLICANT: TICEHURST, JOHN R.;BALTIMORE, DAVID;FEINSTONE,
;STEPHEN M.;PURCELL, ROBERT H.;RACANIELLO, VINCENT R.;
;BAROUDY, BAHIGE M.
;     TITLE OF INVENTION: METHODS OF DETECTING HEPATITIS A VIRUS
;     NUMBER OF SEQUENCES: 4
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/788,262
;       FILING DATE: 06-NOV-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 256,135
;       FILING DATE: 06-OCT-1988
;       APPLICATION NUMBER: 654,942
;       FILING DATE: 27-SEP-1984
;       APPLICATION NUMBER: 537,911
;       FILING DATE: 30-SEP-1983
;SEQ ID NO:2:
;       LENGTH: 1091
5516630-2


  Query Match           100.0%;  Score 107;  DB 6;  Length 1091;
  Best Local Similarity  100.0%;  Pred. No. 4e-10;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 SHIECRKPYKELRLEVGKQR 20
           ||||||||||||||||||||
Db    1029 SHIECRKPYKELRLEVGKQR 1048


RESULT   2
US-08-475-886-2
; Sequence 2, Application US/08475886A
; Patent No. 6113912
; GENERAL INFORMATION:
;  APPLICANT: FUNKHOUSER, ANN W
;  APPLICANT: EMERSON, SUZANNE U
;  APPLICANT: PURCELL, ROBERT H
;  APPLICANT: D'HONDT, ERIC
;  TITLE OF INVENTION: HEPATITIS A VIRUS VACCINES
;  FILE REFERENCE: 20264262US2
;  CURRENT APPLICATION NUMBER: US/08/475,886A
;  CURRENT FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 07/947,338
;  EARLIER FILING DATE: 1992-09-18
;  EARLIER APPLICATION NUMBER: 08/397,232
;  EARLIER FILING DATE: 1995-03-10
;  NUMBER OF SEQ ID NOS: 6
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;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 2227
;   TYPE: PRT
;   ORGANISM: WILD-TYPE HUMAN HEPATITIS A VIRUS, STRAIN HM-175
US-08-475-886-2


  Query Match             100.0%;  Score 107;  DB 4;  Length 2227;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-10;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db    792 SHIECRKPYKELRLEVGKQR 811


RESULT   3
US-08-475-886-4
; Sequence 4, Application US/08475886A
; Patent No. 6113912
; GENERAL INFORMATION:
;  APPLICANT: FUNKHOUSER, ANN W
;  APPLICANT: EMERSON, SUZANNE U
;  APPLICANT: PURCELL, ROBERT H
;  APPLICANT: D'HONDT, ERIC
;  TITLE OF INVENTION: HEPATITIS A VIRUS VACCINES
;  FILE REFERENCE: 20264262US2
;  CURRENT APPLICATION NUMBER: US/08/475,886A
;  CURRENT FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 07/947,338
;  EARLIER FILING DATE: 1992-09-18
;  EARLIER APPLICATION NUMBER: 08/397,232
;  EARLIER FILING DATE: 1995-03-10
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 2227
;   TYPE: PRT
;   ORGANISM: Attenuated HAV (Pass 35), strain HM-175
US-08-475-886-4


  Query Match             100.0%;  Score 107;  DB 4;  Length 2227;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-10;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db    792 SHIECRKPYKELRLEVGKQR 811


RESULT   4
US-08-475-886-6
; Sequence 6, Application US/08475886A
; Patent No. 6113912
; GENERAL INFORMATION:
;  APPLICANT: FUNKHOUSER, ANN W
;  APPLICANT: EMERSON, SUZANNE U
;  APPLICANT: PURCELL, ROBERT H
;  APPLICANT: D'HONDT, ERIC
;  TITLE OF INVENTION: HEPATITIS A VIRUS VACCINES
;  FILE REFERENCE: 20264262US2
;  CURRENT APPLICATION NUMBER: US/08/475,886A
;  CURRENT FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 07/947,338
;  EARLIER FILING DATE: 1992-09-18
;  EARLIER APPLICATION NUMBER: 08/397,232
;  EARLIER FILING DATE: 1995-03-10
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 2227
;   TYPE: PRT
;   ORGANISM: Attenuated (4380) HAV, strain HM-175
US-08-475-886-6


  Query Match             100.0%;  Score 107;  DB 4;  Length 2227;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-10;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db    792 SHIECRKPYKELRLEVGKQR 811


RESULT   5
US-08-397-232-2
; Sequence 2, Application US/08397232A
; Patent No. 6180110
; GENERAL INFORMATION:
;  APPLICANT: FUNKHOUSER, ANN W
;  APPLICANT: EMERSON, SUZANNE U
;  APPLICANT: PURCELL, ROBERT H
;  APPLICANT: D'HONDT, ERIC
;  TITLE OF INVENTION: HEPATITIS A VIRUS VACCINES
;  FILE REFERENCE: 20264262US1
;  CURRENT APPLICATION NUMBER: US/08/397,232A
;  CURRENT FILING DATE: 1995-04-17
;  EARLIER APPLICATION NUMBER: 07/947,338
;  EARLIER FILING DATE: 1992-09-18
;  EARLIER APPLICATION NUMBER: PCT/US93/08610
;  EARLIER FILING DATE: 1993-09-17
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 2227
;   TYPE: PRT
;   ORGANISM: WILD-TYPE HUMAN HEPATITIS A VIRUS, STRAIN HM-175
US-08-397-232-2


  Query Match             100.0%;  Score 107;  DB 4;  Length 2227;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-10;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SHIECRKPYKELRLEVGKQR 20
          ||||||||||||||||||||
Db    792 SHIECRKPYKELRLEVGKQR 811


RESULT   6
US-08-397-232-4
; Sequence 4, Application US/08397232A
; Patent No. 6180110
; GENERAL INFORMATION:
;  APPLICANT: FUNKHOUSER, ANN W
;  APPLICANT: EMERSON, SUZANNE U
;  APPLICANT: PURCELL, ROBERT H
;  APPLICANT: D'HONDT, ERIC
;  TITLE OF INVENTION: HEPATITIS A VIRUS VACCINES
;  FILE REFERENCE: 20264262US1
;  CURRENT APPLICATION NUMBER: US/08/397,232A
;  CURRENT FILING DATE: 1995-04-17
;  EARLIER APPLICATION NUMBER: 07/947,338
;  EARLIER FILING DATE: 1992-09-18
;  EARLIER APPLICATION NUMBER: PCT/US93/08610
;  EARLIER FILING DATE: 1993-09-17
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 2227
;   TYPE: PRT
;   ORGANISM: Attenuated (4380) HAV, strain HM-175
US-08-397-232-4
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  Query Match            100.0%;  Score 107;  DB 4;  Length 2227;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-10;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 SHIECRKPYKELRLEVGKQR 20
           ||||||||||||||||||||
Db     792 SHIECRKPYKELRLEVGKQR 811


RESULT   7
US-08-087-016-2
; Sequence 2, Application US/08087016
; Patent No. 5430135
;  GENERAL INFORMATION:
;    APPLICANT:  NAINAN, OMANA V.
;    APPLICANT:  MARGOLIS, HAROLD S.
;    APPLICANT:  ROBERTSON, BETTY H.
;    APPLICANT:  BRINTON, MARGO H.
;    APPLICANT:  EBERT, JAMES W.
;    TITLE OF INVENTION:  HEPATITIS A VIRUS VACCINE
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CUSHMAN, DARBY & CUSHMAN
;      STREET:  1615 L Street N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/087,016
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/678,828
;      FILING DATE:  03-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SCOTT, WATSON T.
;      REGISTRATION NUMBER:  26,581
;      REFERENCE/DOCKET NUMBER:  WTS/5683/83834/SRL
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 861-3000
;      TELEFAX:  (202) 822-0944
;      TELEX:  6714627 CUSH
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  839 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-087-016-2


  Query Match            79.0%;  Score 84.5;  DB 1;  Length 839;
  Best Local Similarity   90.0%;  Pred. No. 2.1e-06;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    1;  Gaps    1;

Qy       1 SHIECRKPYKELRLEVGKQR 20
           |||| :|||||||||||||||
Db     792 SHIE-KKPYKELRLEVGKQR 810


RESULT   8
US-09-150-460B-11
; Sequence 11, Application US/09150460B
; Patent No. 6190882
; GENERAL INFORMATION:
;  APPLICANT:  Lee, Cheng-Chi
;  APPLICANT:  Albrecht, Urs
;  APPLICANT:  Eichele, Gregor
;  APPLICANT:  Sun, Zhong Sheng
;  TITLE OF INVENTION:  Mammalian Circadian Rhythym-Like Gene
;  FILE REFERENCE:  D6039
;  CURRENT APPLICATION NUMBER: US/09/150,460B
;  CURRENT FILING DATE:  1998-09-09
;  PRIOR APPLICATION NUMBER:  US 60/058,256
;  PRIOR FILING DATE:  1997-09-09
;  NUMBER OF SEQ ID NOS:  21
; SEQ ID NO 11
;   LENGTH: 1127
;   TYPE: PRT
;   ORGANISM: D. melanogaster Period
;   FEATURE:
;   OTHER INFORMATION: Predicted protein sequence compared with RIGUI 4.7
US-09-150-460B-11


  Query Match            40.2%;  Score 43;  DB 4;  Length 1127;
  Best Local Similarity   77.8%;  Pred. No. 35;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 ECRKPYKEL 12
           || |||:||
Db     392 ECSKPYREL 400


RESULT   9
PCT-US91-08177-3
; Sequence 3, Application PC/TUS9108177
;  GENERAL INFORMATION:
;    APPLICANT:  Samal, Siba K
;    TITLE OF INVENTION:  Bovine Respiratory Syncytial Virus Genes
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Venable, Baetjer, Howard & Civiletti
;      STREET:  1201 New York Avenue N.W., suite 1000
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/08177
;      FILING DATE:  19911104
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/608,937
;      FILING DATE:  05-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Highet, David W
;      REGISTRATION NUMBER:  30,265
;      REFERENCE/DOCKET NUMBER:  20509-96711
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-962-4854
;      TELEFAX:  202-962-8300
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  391 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US91-08177-3


  Query Match            38.3%;  Score 41;  DB 5;  Length 391;
  Best Local Similarity   50.0%;  Pred. No. 24;
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  Matches    8;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3 IECRKPYKELRLEVGK 18
           || || ||::  |:|:
Db     129 IESRKSYKKMLKEMGE 144


RESULT  10
US-08-469-486-52
; Sequence 52, Application US/08469486
; Patent No. 5739281
;  GENERAL INFORMATION:
;    APPLICANT:  Thoegersen, Hans Christian
;    APPLICANT:  Holtet, Thor Las
;    APPLICANT:  Etzerodt, Michael
;    TITLE OF INVENTION:  Improved method for the refolding of
;    TITLE OF INVENTION:  proteins
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version
;      SOFTWARE:  #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,486
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/192,060
;      FILING DATE:  February 4, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul T. Clark
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  06363/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617 542 5070
;      TELEFAX:  617 542 8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  52:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4544 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-469-486-52


  Query Match             38.3%;  Score 41;  DB 1;  Length 4544;
  Best Local Similarity   56.2%;  Pred. No. 3.6e+02;
  Matches    9;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       5 CRKPYKELRLEVGKQR 20
           |:||  || |  || |
Db     519 CKKPEHELFLVYGKGR 534


RESULT  11
US-08-469-658-52
; Sequence 52, Application US/08469658
; Patent No. 5917018
;  GENERAL INFORMATION:
;    APPLICANT:  Th egersen, Hans Christian
;    APPLICANT:  Holtet, Thor Las
;    APPLICANT:  Etzerodt, Michael
;    TITLE OF INVENTION:  IMPROVED METHOD FOR THE REFOLDING OF
;    TITLE OF INVENTION:  PROTEINS
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version
;      SOFTWARE:  #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,658
;      FILING DATE:  June 5, 1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/192,060
;      FILING DATE:  February 4, 1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul T. Clark
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  06363/002002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617 542 5070
;      TELEFAX:  617 542 8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  52:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4544 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-469-658-52


  Query Match             38.3%;  Score 41;  DB 2;  Length 4544;
  Best Local Similarity   56.2%;  Pred. No. 3.6e+02;
  Matches    9;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       5 CRKPYKELRLEVGKQR 20
           |:||  || |  || |
Db     519 CKKPEHELFLVYGKGR 534


RESULT  12
US-08-406-347A-13
; Sequence 13, Application US/08406347A
; Patent No. 5714374
;  GENERAL INFORMATION:
;    APPLICANT:  ARNOLD, Edward V.
;    APPLICANT:  ARNOLD, Gail F.
;    TITLE OF INVENTION:  CHIMERIC RHINOVIRUSES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenyon & Kenyon
;      STREET:  1025 Connecticut Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.50 inch floppy disk, 1.44 mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1 Windows
;    CURRENT APPLICATION DATA:
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;       APPLICATION NUMBER:  US/08/406,347A
;       FILING DATE:  17-MAR-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/304,635
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/041,790
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/583,335
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Toffenetti, Judith L.
;       REGISTRATION NUMBER:  39,048
;       REFERENCE/DOCKET NUMBER:  1984/46203
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-429-1776
;       TELEFAX:  202-429-0796
;   INFORMATION FOR SEQ ID NO:  13 :
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  24 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-406-347A-13


  Query Match             36.4%;  Score 39;  DB 1;  Length 24;
  Best Local Similarity   33.3%;  Pred. No. 2.5;
  Matches    6;  Conservative    4;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       3 IECRKPYKELRLEVGKQR 20
           | | :||  :|  : : |
Db       5 INCTRPYNNVRRSLSRTR 22


RESULT  13
US-09-393-554-2
; Sequence 2, Application US/09393554
; Patent No. 6210897
; GENERAL INFORMATION:
;  APPLICANT: Andersson, Leif
;  APPLICANT: Kijas, James
;  APPLICANT: Gafvert, Sophie
;  APPLICANT: Wigh-Trowaldh, Gunilla
;  APPLICANT: Hedhammar, Ake
;  TITLE OF INVENTION: IDENTIFICATION OF CANINE LEUKOCYTE ADHESION DEFICIENCY
;  TITLE OF INVENTION: IN DOGS
;  FILE REFERENCE: 201515/1001
;  CURRENT APPLICATION NUMBER: US/09/393,554
;  CURRENT FILING DATE: 1999-09-10
;  EARLIER APPLICATION NUMBER: 60/136,099
;  EARLIER FILING DATE: 1999-05-26
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 344
;   TYPE: PRT
;   ORGANISM: Bos sp.
US-09-393-554-2


  Query Match             36.4%;  Score 39;  DB 4;  Length 344;
  Best Local Similarity   32.1%;  Pred. No. 46;
  Matches    9;  Conservative    3;  Mismatches    4;  Indels   12;  Gaps    1;

Qy       4 ECRKPY------------KELRLEVGKQ 19
             ||: |:            |:   |||||
Db     197 ECQPPFAFRHVLKLTDNSKQFETEVGKQ 224


RESULT  14
5223391-5
;Patent No. 5223391
;     APPLICANT: COEN, DONALD M.;DIGARD, PAUL E.
;     TITLE OF INVENTION: INHIBITIORS OF HERPES SIMPLEX VIRUS
;REPLICATION
;     NUMBER OF SEQUENCES: 9
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/482,634
;       FILING DATE: 21-FEB-1990
;SEQ ID NO:5:
;       LENGTH: 520
5223391-5


  Query Match             36.4%;  Score 39;  DB 6;  Length 520;
  Best Local Similarity   45.0%;  Pred. No. 73;
  Matches    9;  Conservative    4;  Mismatches    5;  Indels    2;  Gaps    1;

Qy       1 SHIECRKPYKELRLEVGKQR 20
           :|:|  | |  | :||| :|
Db     295 AHLEAGKDY--LEIEVGGRR 312


RESULT  15
US-08-680-326-36
; Sequence 36, Application US/08680326
; Patent No. 5925733
;  GENERAL INFORMATION:
;     APPLICANT:  ROSE, TIMOTHY M.
;     APPLICANT:  BOSCH, MARNIX
;     APPLICANT:  STRAND, KURT
;     APPLICANT:  TODARO, GEORGE J.
;     TITLE OF INVENTION:  DNA POLYMERASE OF GAMMA HERPES VIRUSES
;     TITLE OF INVENTION:  ASSOCIATED WITH KAPOSI'S SARCOMA AND RETROPERITONEAL
;     TITLE OF INVENTION:  FIBROMATOSIS
;     NUMBER OF SEQUENCES:  152
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  MORRISON & FOERSTER
;       STREET:  755 Page Mill Road
;       CITY:  Palo Alto
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94304-1018
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/680,326
;       FILING DATE:
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Schiff, J. Michael
;       REGISTRATION NUMBER:  40,253
;       REFERENCE/DOCKET NUMBER:  29938-20001.00
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 813-5600
;       TELEFAX:  (415) 494-0792
;       TELEX:  706141
;   INFORMATION FOR SEQ ID NO:  36:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1235 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-680-326-36


  Query Match             36.4%;  Score 39;  DB 2;  Length 1235;
  Best Local Similarity   45.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    4;  Mismatches    5;  Indels    2;  Gaps    1;

Qy       1 SHIECRKPYKELRLEVGKQR 20
           :|:|  | |  | :||| :|
Db     744 AHLEAGKDY--LEIEVGGRR 761
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Search completed: April 24, 2001, 16:34:58
Job time: 529 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2001, 16:23:11 ; Search time 121.9 Seconds
(without alignments)
9.379 Million cell updates/sec

Title: US-09-171-432A-40
Perfect score: 102
Sequence: 1 PYKELRLEVGKQRLKYAQEE 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0401:*
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2: /SIDS1/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	102	100.0	20	18	W42923	Immunogenic Hepati
2	102	100.0	366	6	P50230	Sequence of hepati
3	102	100.0	854	6	P50287	Sequence encoded b
4	102	100.0	993	6	P50116	Sequence of Hepati
5	102	100.0	993	6	P50231	Sequence encoded b
6	102	100.0	1077	20	W95559	A partial hepatiti
7	102	100.0	1091	14	R32426	Translated from 5'
8	102	100.0	2227	11	R05697	Attenuated hepatit
9	102	100.0	2227	18	W34074	Hepatitis A virus
10	102	100.0	2227	21	B18607	Amino acid sequenc
11	102	100.0	2227	21	B18608	Amino acid sequenc
12	102	100.0	2227	21	B18609	Amino acid sequenc
13	99	97.1	2227	7	P60066	Sequence of viral
14	94	92.2	839	12	R15629	Capsid region of c
15	67	65.7	20	18	W42922	Immunogenic Hepati
16	45	44.1	20	18	W42924	Immunogenic Hepati
17	45	44.1	25	18	W42930	Immunogenic Hepati
18	45	44.1	124	20	Y11920	Human 5' EST secre
19	45	44.1	214	20	Y34690	Chlamydia pneumoni
20	42	41.2	411	21	G39793	Arabidopsis thalia
21	42	41.2	452	21	G39792	Arabidopsis thalia
22	41	40.2	68	18	W09415	Human G protein ga
23	41	40.2	68	18	W09417	Human G protein ga
24	41	40.2	68	19	W61906	Human G protein ga
25	41	40.2	68	20	Y17986	Human G protein ga
26	41	40.2	68	20	Y14069	Human CBLAEH07 pro
27	41	40.2	79	21	B43432	Human cancer assoc
28	41	40.2	88	21	G00169	Human secreted pro
29	41	40.2	147	17	R88419	Human 5 lipoxygena
30	41	40.2	161	21	B33220	Eucalyptus grandis
31	41	40.2	187	21	B53341	Human colon cancer
32	40.5	39.7	795	21	Y70962	Rat Ras signalling
33	40	39.2	189	20	Y18062	S. pneumoniae pth
34	40	39.2	189	20	Y18063	S. pneumoniae pth
35	40	39.2	203	21	B51986	Human secreted pro
36	40	39.2	272	21	B54209	Human pancreatic c
37	40	39.2	287	21	Y95447	Putative human des
38	40	39.2	306	19	W84153	Human desaturase e
39	40	39.2	306	20	W95511	Amino acid sequenc
40	40	39.2	306	20	W85132	A desaturase enzym
41	40	39.2	306	21	Y84700	Amino acid sequenc
42	40	39.2	306	21	Y92615	Human desaturase h
43	40	39.2	328	21	Y95449	Human delta-5-desa
44	40	39.2	444	21	B41998	Human ORFX ORF1762
45	40	39.2	444	21	Y97538	Human fatty acid d

ALIGNMENTS

RESULT 1
W42923
ID W42923 standard; peptide; 20 AA.
XX
AC W42923;
XX
DT 28-APR-1998 (first entry)
XX
DE Immunogenic Hepatitis A virus peptide YK-1316.
XX
KW Immunogenic peptide; immunogenic epitope; P2A protein;
KW immune response; antibody.
XX
OS Synthetic.
OS Hepatitis A virus.
XX
PN WO9740147-A1.
XX
PD 30-OCT-1997.
XX
PF 18-APR-1997; 97WO-US06891.
XX
PR 19-APR-1996; 96US-0015644.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Fields HA, Khudyakov YE;
XX
DR WPI; 1997-535831/49.
XX
PT Immunogenic Hepatitis A Virus (HAV) peptide(s) - used to induce an
PT immune response to HAV in a mammal or to detect the presence of
PT antibodies against HAV in a mammal
XX

```
PS   Claim 18; Page 112; 140pp; English.
XX
CC   Peptides W42922-30 are immunogenic peptides corresponding to immunogenic
CC   epitopes of the Hepatitis A virus (HAV). The peptides are substantially
CC   similar to a portion of the amino acid sequence of the P2A protein of HAV
CC   corresponding to amino acids 792-980. The present peptide is derived
CC   from amino acids 799-818, and has a reactivity of 41.7% with acute sera.
CC   Compositions containing the peptides can be used to induce an immune
CC   response to HAV in a mammal. The peptides can also be used to detect the
CC   presence of antibodies against HAV in mammalian serum. The peptides can
CC   also be used to make an antibody against HAV by administering the peptide
CC   to a mammal.
XX
SQ   Sequence   20 AA;


  Query Match             100.0%;  Score 102;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-10;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db      1 pykelrlevgkqrlkyaqee 20


RESULT   2
P50230
ID   P50230 standard; Protein; 366 AA.
XX
AC   P50230;
XX
DT   28-NOV-1991  (first entry)
XX
DE   Sequence of hepatitis A virus (HAV) surface protein (VP-1).
XX
KW   Hepatitis A virus vaccine; immunisation; monoclonal antibody;
KW   diagnostic assay.
XX
OS   Hepatitis A virus.
XX
PN   EP138704-A.
XX
PD   24-APR-1985.
XX
PF   09-OCT-1984;   84EP-0402025.
XX
PR   02-MAR-1984;   84US-0585942.
PR   14-OCT-1983;   83US-0541836.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Hughes JV,  Scolnick EM,  Tomassini JE;
XX
DR   WPI; 1985-100818/17.
DR   N-PSDB; N50274.
XX
PT   New hepatitis A virus surface protein - useful for binding to
PT   neutralising antibodies to the virus
XX
PS   Claim 21; Page 46-48; 49pp; English.
XX
CC   VP1 is isolated by solubilisation of the intact virus in an aq.
CC   anionic surfactant and a reducing agent. The viral proteins are sepd.
CC   and the protein of molecular wt. 33000 daltons is sepd.
XX
SQ   Sequence   366 AA;


  Query Match             100.0%;  Score 102;  DB 6;  Length 366;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db    308 pykelrlevgkqrlkyaqee 327


RESULT   3
P50287
ID   P50287 standard; Protein; 854 AA.
XX
AC   P50287;
XX
DT   30-NOV-1991  (first entry)
XX
DE   Sequence encoded by hepatitis A virus (HAV) cDNA from near the
DE   genome 5' terminus to the end of the area corresponding to the
DE   capsid protein region of poliovirus RNA.
XX
KW   Hepatitis A virus assay; antigen; antibody.
XX
OS   Hepatitis A virus.
XX
PN   WO8501517-A.
XX
PD   11-APR-1985.
XX
PF   27-SEP-1984;   84WO-US01552.
XX
PR   30-SEP-1983;   83US-0537911.
XX
PA   (MASI ) MASSACHUSETTS INST TECH.
XX
PI   Ticechurst JR,  Baltimore D,  Feinstone SM,  Purcell RH;
PI   Racaniello VR;
XX
DR   WPI; 1985-098846/16.
DR   N-PSDB; N50330.
XX
PT   New hepatitis A virus CDNA - useful in assays for the virus and
PT   for prodn. of the viral antigen and antibodies to it
XX
PS   Example; Fig 7; 60pp; English.
XX
CC   The inventors claim HAV cDNA and a method for producing it, whereby
CC   large amts. can be obtd. economically. The cDNA is useful in the
CC   assay for detection of HAV quickly and easily and with high
CC   sensitivity and specificity. The HAV cDNA is also used in the prodn.
CC   of HAV antigen or antibodies to it. The antibodies may be monoclonal.
XX
SQ   Sequence   854 AA;


  Query Match             100.0%;  Score 102;  DB 6;  Length 854;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db    799 pykelrlevgkqrlkyaqee 818


RESULT   4
P50116
ID   P50116 standard; Protein; 993 AA.
XX
AC   P50116;
XX
DT   30-SEP-1991  (first entry)
XX
DE   Sequence of Hepatitis A virus (HAV) immunogenic peptides
DE   VP-1, VP-2, VP-3 and VP-4.
XX
KW   Antigenic protein; immunogen; vaccine.
XX
OS   Hepatitis A virus (strain CR326).
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```
XX
PN   EP154587-A.
XX
PD   11-SEP-1985.
XX
PF   27-FEB-1985;   85EP-0400369.
XX
PR   02-MAR-1984;   84US-0585818.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Linemeyer DL,  Menke JG,  Reuben RG,  Mitra SW;
XX
DR   WPI; 1985-224964/37.
DR   N-PSDB; N50139.
XX
PT   New nucleotide sequences coding for hepatitis A virus antigens -
PT   useful for eliciting normal immune response and in vaccines for
PT   protecting against the virus
XX
PS   Example; Page 11-17; 32pp; English.
XX
CC   Within the sequence in N50139 is encoded the information necessary
CC   to make the antigenic proteins of HAV. The sequences encoding for
CC   the structural proteins begin at base 403. The key sub-unit
CC   sequences within VP-1, designated Sequences I,II,III,IV, and V,
CC   start, respectively at 1882, 1963, 1999, 2146, 2347. Other
CC   nucleotide sequences which are valuable as encoding antigenic
CC   proteins are the sequences from base 1749 to base 2722; from base
CC   1487 to base 2980 and from base 1644 to base 2722. The sequence from
CC   base 1749 to base 2722 is esp. valuable as a vector for producing
CC   antigen protein. Sequences II-V are claimed. X in P50116 denotes the
CC   translation of a stop codon.
XX
SQ   Sequence   993 AA;


  Query Match             100.0%;  Score 102;  DB 6;  Length 993;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db    935 pykelrlevgkqrlkyaqee 954


RESULT   5
P50231
ID   P50231 standard; Protein; 993 AA.
XX
AC   P50231;
XX
DT   28-NOV-1991  (first entry)
XX
DE   Sequence encoded by partial sequence of hepatitis A virus (HAV),
DE   including surface protein (VP-1).
XX
KW   Hepatitis A virus vaccine; immunisation; monoclonal antibody;
KW   diagnostic assay.
XX
OS   Hepatitis A virus.
XX
FH   Key             Location/Qualifiers
FT   Protein         628..993
FT                   /note= "claimed; X denotes translated stop codons
FT                          and unspecified triplets"
XX
PN   EP138704-A.
XX
PD   24-APR-1985.
XX
PF   09-OCT-1984;   84EP-0402025.
XX
PR   02-MAR-1984;   84US-0585942.
PR   14-OCT-1983;   83US-0541836.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Hughes JV,  Scolnick EM,  Tomassini JE;
XX
DR   WPI; 1985-100818/17.
DR   N-PSDB; N50274.
XX
PT   New hepatitis A virus surface protein - useful for binding to
PT   neutralising antibodies to the virus
XX
PS   Disclosure; Page 17-23; 49pp; English.
XX
CC   VP1 is isolated by solubilisation of the intact virus in an aq.
CC   anionic surfactant and a reducing agent. The viral proteins are sepd.
CC   and the protein of molecular wt. 33000 daltons is sepd.
XX
SQ   Sequence   993 AA;


  Query Match             100.0%;  Score 102;  DB 6;  Length 993;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db    935 pykelrlevgkqrlkyaqee 954


RESULT   6
W95559
ID   W95559 standard; Protein; 1077 AA.
XX
AC   W95559;
XX
DT   28-APR-1999  (first entry)
XX
DE   A partial hepatitis A virus (HAV) protein.
XX
KW   Hepatitis A virus protein; HAV; P2 region;
KW   cell-culture-adapted HAV strain; infection; accelerated growth.
XX
OS   Hepatitis A virus.
XX
PN   US5849562-A.
XX
PD   15-DEC-1998.
XX
PF   06-JUN-1995;   95US-0468926.
XX
PR   06-NOV-1991;   91US-0788262.
PR   30-SEP-1983;   83US-0537911.
PR   27-SEP-1984;   84US-0654942.
PR   06-OCT-1988;   88US-0256135.
PR   06-JUN-1995;   95US-0468926.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Emerson SU,  Purcell RH;
XX
DR   WPI; 1999-094412/08.
DR   N-PSDB; X01006.
XX
PT   Chimeric hepatitis A virus strains - with P2 region from
PT   cell-culture-adapted strain in wild-type genome
XX
PS   Disclosure; Fig 7A-L; 36pp; English.
XX
CC   The present sequence represents a partial hepatitis A virus (HAV)
CC   protein. The specification describes a DNA construct consisting
CC   of a wild-type HAV genome in which the P2 region is replaced by the
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CC   P2 region from a cell-culture-adapted HAV strain. The construct is
CC   used to demonstrate that mutations in the P2 region of a
CC   cell-culture-adapted HAV strain are sufficient for establishment of
CC   infection and accelerated growth in cell culture.
XX
SQ   Sequence   1077 AA;


  Query Match           100.0%;  Score 102;  DB 20;  Length 1077;
  Best Local Similarity  100.0%;  Pred. No. 3e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db   1022 pykelrlevgkqrlkyaqee 1041


RESULT   7
R32426
ID   R32426 standard; Protein; 1091 AA.
XX
AC   R32426;
XX
DT   10-JUN-1993  (first entry)
XX
DE   Translated from 5' region of Hepatitis A Virus genomic clone.
XX
KW   HAV HM-175; chronic liver disease; picornavirus.
XX
OS   Hepatitis A Virus.
XX
FH   Key             Location/Qualifiers
FT   Region          238..1091
FT                   /label= ORF
FT                   /note= "second putative initiation codon at
FT                          position 240"
FT   Region          1..711
FT                   /note= "X's correspond to nonsense codons,
FT                          i.e. this region is not an ORF"
XX
PN   US7788262-A.
XX
PD   15-DEC-1992.
XX
PF   30-SEP-1983;   83US-0536911.
XX
PR   27-SEP-1984;   84US-0654942.
PR   06-OCT-1988;   88US-0256135.
PR   30-SEP-1983;   83US-0536911.
PR   06-NOV-1991;   91US-0788262.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX
PI   Baltimore D,  Feinstone SM;
PI    Purcell RH,  Racaniello VR,  Ticehurst JR;
XX
DR   WPI; 1993-067429/08.
DR   N-PSDB; Q36934.
XX
PT   Hepatitis A virus cDNA prodn. - for diagnostic use and for prodn.
PT   of antigen and antibodies
XX
PS   Disclosure; Fig 7; 65pp; English.
XX
CC   HAV virion RNA was extracted from the livers of marmosets which had
CC   been inoculated with HAV (the HAV had previously been passaged twice
CC   in marmosets). The RNA was used to prepare ds cDNA clones by
CC   standard methods. Clones contg. inserts which hybridised to RNA from
CC   HAV-infected African Green Monkey Kidney cells were selected for
CC   further analysis. A 7.4kb restriction map (about 99% of the HAV
CC   genome) was constructed from 5 overlapping inserts. The sequence of
CC   the first 3.3kb (approx.) from the 5'-terminus was determined. An
CC   amino acid sequence was decoded from the entire clone and an open
CC   reading frame was identified starting at position 238. A comparison
CC   of the predicted HAV amino acid sequences with the known capsid
CC   protein sequences of other picornaviruses (poliovirus, foot and
CC   mouth disease virus and encephalomyelitis virus) revealed areas of
CC   local homology.
XX
SQ   Sequence   1091 AA;


  Query Match           100.0%;  Score 102;  DB 14;  Length 1091;
  Best Local Similarity  100.0%;  Pred. No. 3.1e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db   1036 pykelrlevgkqrlkyaqee 1055


RESULT   8
R05697
ID   R05697 standard; protein; 2227 AA.
XX
AC   R05697;
XX
DT   15-AUG-1990  (first entry)
XX
DE   Attenuated hepatitis A virus.
XX
KW   Hepatitis A virus; vaccine; attenuated.
XX
OS   Hepatitis A virus, strain HM-175.
XX
FH   Key             Location/Qualifiers
FT   Region          1..23
FT                   /label=VP4 = 1A
FT   Region          24..245
FT                   /label=VP2 = 1B
FT   Region          246..491
FT                   /label=VP3 = 1C
FT   Region          492..791
FT                   /label=VP1 = 1D
FT   Region          792..980
FT                   /label=2A
FT   Region          981..1087
FT                   /label=2B
FT   Region          1088..1422
FT                   /label=2C
FT   Region          1423..1496
FT                   /label=3A
FT   Region          1497..1519
FT                   /label=3B = VPg
FT   Region          1520..1738
FT                   /label=3C
FT   Region          1739..2227
FT                   /label=3D
XX
PN   US4894228-A.
XX
PD   16-JAN-1990.
XX
PF   12-JUL-1988;   88US-0217824.
XX
PR   12-JUL-1988;   88US-0217824.
PR   12-JUL-1988;   88US-0652967.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN.
XX
PI   Purcell RH,  Ticehurst JR,  Cohen I,  Emerson SU,  Feinstone SM;
PI   Daemer RJ,  Gust ID;
XX
DR   WPI; 1990-075557/10.
DR   N-PSDB; Q03512.
XX
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PT   Vaccine against hepatitis A virus  infection -  comprises novel
PT   attenuated hepatitis A virus strain.
XX
PS   Claim 1; Fig 1; 18pp; English.
XX
CC   The attenuated HAV is useful for inducing protective immunity against
CC   HAV. This strain (Pass 35) differs from the wild type HAV HM-175 by
CC   several nucleotide changes distributed throughout the genome, is
CC   attenuated for chimpanzees, elicits serum neutralising antibodies, and is
CC   suitable for use as an HAV vaccine. It is noted that not all the changes
CC   are necessary for attenuation and use as a vaccine.
XX
SQ   Sequence   2227 AA;


  Query Match            100.0%;  Score 102;  DB 11;  Length 2227;
  Best Local Similarity  100.0%;  Pred. No. 6.6e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db    799 pykelrlevgkqrlkyaqee 818


RESULT   9
W34074
ID   W34074 standard; Protein; 2227 AA.
XX
AC   W34074;
XX
DT   27-APR-1998  (first entry)
XX
DE   Hepatitis A virus HM-175 protein sequence.
XX
KW   HAV; attenuation; 2C protein; 2C chimeric hepatitis A virus;
KW   infection; vaccine.
XX
OS   Hepatitis A virus HM-175.
XX
FH   Key             Location/Qualifiers
FT   Protein         1..23
FT                   /label= VP4
FT   Protein         24..245
FT                   /label= VP2
FT   Protein         246..491
FT                   /label= VP3
FT   Protein         492..791
FT                   /label= VP1
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FT                   /label= 3A
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FT                   /label= 3B
FT   Protein         1520..1738
FT                   /label= 3C
FT   Protein         1739..2227
FT                   /label= 3D
XX
PN   WO9740166-A2.
XX
PD   30-OCT-1997.
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PF   18-APR-1997;   97WO-US06506.
XX
PR   19-APR-1996;   96US-0015642.
XX
PA   (USSH ) US SEC DEPT HEALTH.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Emerson SU,  Purcell RH,  Raychaudhuri G;
XX
DR   WPI; 1997-535850/49.
DR   N-PSDB; T93023.
XX
PT   Human attenuated HAV genome containing simian HAV 2C gene - useful
PT   as vaccines against HAV infection
XX
PS   Disclosure; Fig 13A-D; 66pp; English.
XX
CC   This protein sequence is encoded by the human hepatitis A virus
CC   (HAV) HM-175 wild-type genome (see T93023).  Attenuated strain
CC   HAV/7 is obtained by passage of HM-175 in African Green Monkey
CC   kidney cells.  A claimed DNA construct (I) comprises a genome of
CC   HAV, where the genome is a human attenuated HAV genome in which a
CC   region of the 2C gene has been replaced by a corresponding region
CC   from a 2C gene of a simian AGM-27 HAV genome (see T93024).  The
CC   region of the 2C gene from AGM-27 contained in the construct
CC   preferably encodes amino acids 120-328 of the 2C protein, amino
CC   acids 1-121 or amino acids 1-328.  Also claimed are: (1) an RNA
CC   transcript of (I); (2) a cell transfected with (I) or the RNA
CC   transcript of (1); (3) a HAV genome as above; (4) antibodies to the
CC   HAV of (3); and (5) a host cell containing the HAV of (3).  (I) or
CC   its RNA transcript, can be used as a vaccine for preventing HAV in
CC   a mammal.  (I) or the RNA transcript can also be used to stimulate
CC   the production of protective antibodies in the mammal.
XX
SQ   Sequence   2227 AA;


  Query Match            100.0%;  Score 102;  DB 18;  Length 2227;
  Best Local Similarity  100.0%;  Pred. No. 6.6e-08;
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Qy      1 PYKELRLEVGKQRLKYAQEE 20
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Db    799 pykelrlevgkqrlkyaqee 818


RESULT  10
B18607
ID   B18607 standard; Protein; 2227 AA.
XX
AC   B18607;
XX
DT   15-JAN-2001  (first entry)
XX
DE   Amino acid sequence of wild type Hepatitis A virus strain HM-175.
XX
KW   HAV; strain HM-174; MRC-5 cell; live vaccine; hepatitis A infection.
XX
OS   Hepatitis A virus.
XX
PN   US6113912-A.
XX
PD   05-SEP-2000.
XX
PF   07-JUN-1995;   95US-0475886.
XX
PR   18-SEP-1992;   92US-0947338.
PR   17-SEP-1993;   93WO-US08610.
PR   10-MAR-1995;   95US-0397232.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   D'Hondt E,  Purcell RH,  Emerson SU,  Funkhouser AW;
XX
DR   WPI; 2000-586464/55.
DR   N-PSDB; A75476.
XX
PT   Novel live hepatitis A virus adapted to growth in human fibroblast cell
PT   line useful as vaccine for protecting humans against hepatitis A virus
```

```
PT   infection, has modified genome compared to wild type  -
XX
PS   Disclosure; Fig 6A-K; 72pp; English.
XX
CC   The present sequence is derived from a wild type hepatitis A virus
CC   (HAV) strain HM-174. The sequence is modified to produce HAV which
CC   are adapted to growth in the human fibroblast-like cell line MRC-5.
CC   The HAV is able to propagate in MRC-5 cells and retain appropriate
CC   attenuation. It is useful as a live vaccine for prophylaxis of
CC   hepatitis A in humans and other primates.
XX
SQ   Sequence   2227 AA;


  Query Match            100.0%;  Score 102;  DB 21;  Length 2227;
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Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db    799 pykelrlevgkqrlkyaqee 818


RESULT  11
B18608
ID   B18608 standard; Protein; 2227 AA.
XX
AC   B18608;
XX
DT   15-JAN-2001  (first entry)
XX
DE   Amino acid sequence of passage 35 Hepatitis A virus called P-35.
XX
KW   HAV; strain HM-174; MRC-5 cell; live vaccine; hepatitis A infection;
KW   P-35 virus.
XX
OS   Hepatitis A virus.
XX
PN   US6113912-A.
XX
PD   05-SEP-2000.
XX
PF   07-JUN-1995;   95US-0475886.
XX
PR   18-SEP-1992;   92US-0947338.
PR   17-SEP-1993;   93WO-US08610.
PR   10-MAR-1995;   95US-0397232.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   D'Hondt E,  Purcell RH,  Emerson SU,  Funkhouser AW;
XX
DR   WPI; 2000-586464/55.
DR   N-PSDB; A75477.
XX
PT   Novel live hepatitis A virus adapted to growth in human fibroblast cell
PT   line useful as vaccine for protecting humans against hepatitis A virus
PT   infection, has modified genome compared to wild type  -
XX
PS   Disclosure; Columns 67-78; 72pp; English.
XX
CC   The present sequence is derived from passage 35 of a wild type
CC   hepatitis A virus (HAV) strain HM-174. The resulting virus is
CC   designated P-35 virus. The sequence is modified to produce HAV which
CC   are adapted to growth in the human fibroblast-like cell line MRC-5.
CC   The HAV is able to propagate in MRC-5 cells and retain appropriate
CC   attenuation. It is useful as a live vaccine for prophylaxis of
CC   hepatitis A in humans and other primates.
XX
SQ   Sequence   2227 AA;


  Query Match            100.0%;  Score 102;  DB 21;  Length 2227;
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Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db    799 pykelrlevgkqrlkyaqee 818


RESULT  12
B18609
ID   B18609 standard; Protein; 2227 AA.
XX
AC   B18609;
XX
DT   15-JAN-2001  (first entry)
XX
DE   Amino acid sequence of live attenuated Hepatitis A virus 4380.
XX
KW   HAV; strain HM-174; MRC-5 cell; live vaccine; hepatitis A infection;
KW   HAV 4380.
XX
OS   Hepatitis A virus.
XX
PN   US6113912-A.
XX
PD   05-SEP-2000.
XX
PF   07-JUN-1995;   95US-0475886.
XX
PR   18-SEP-1992;   92US-0947338.
PR   17-SEP-1993;   93WO-US08610.
PR   10-MAR-1995;   95US-0397232.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   D'Hondt E,  Purcell RH,  Emerson SU,  Funkhouser AW;
XX
DR   WPI; 2000-586464/55.
DR   N-PSDB; A75478.
XX
PT   Novel live hepatitis A virus adapted to growth in human fibroblast cell
PT   line useful as vaccine for protecting humans against hepatitis A virus
PT   infection, has modified genome compared to wild type  -
XX
PS   Disclosure; Columns 93-104; 72pp; English.
XX
CC   The present sequence is derived from a live attenuated hepatitis A
CC   virus (HAV) of the invention, designated HAV 4380. The sequence is
CC   produced by modifying wild type HAV strain HM-174. The HAV of the
CC   invention are adapted to growth in the human fibroblast-like cell
CC   line MRC-5. The HAV is able to propagate in MRC-5 cells and retain
CC   appropriate attenuation. It is useful as a live vaccine for prophylaxis
CC   of hepatitis A in humans and other primates.
XX
SQ   Sequence   2227 AA;


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Qy      1 PYKELRLEVGKQRLKYAQEE 20
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Db    799 pykelrlevgkqrlkyaqee 818


RESULT  13
P60066
ID   P60066 standard; Protein; 2227 AA.
XX
AC   P60066;
XX
DT   26-JUN-1991  (first entry)
```

```
XX
DE   Sequence of viral L434 polypeptide encoded by the complete
DE   nucleotide sequence of the HAV genome.
XX
KW   Diagnosis; vaccine; passive immunotherapy.
XX
OS   Hepatitis A virus.
XX
FH   Key             Location/Qualifiers
FT   Region          1..245
FT                   /label= P1.1A
FT   Region          246..491
FT                   /label= 1B
FT   Region          492..836
FT                   /label= 1C
FT   Region          837..980
FT                   /label= P2.2A
FT   Region          981..1076
FT                   /label= 2B
FT   Region          1077..1422
FT                   /label= 2C
FT   Region          1423..1484
FT                   /label= P3.3A
FT   Region          1485..1507
FT                   /label= 3B
FT   Region          1508..1678
FT                   /label= 3C
FT   Region          1679..2227
FT                   /label= 3D
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PN   EP199480-A.
XX
PD   29-OCT-1986.
XX
PF   03-APR-1986;   86EP-0302465.
XX
PR   03-APR-1985;   85US-0719329.
XX
PA   (CHIR-) CHIRON CORP.
XX
PI   Dina D,  Potter SJ,  Vannest GA,  Caput D;
XX
DR   WPI; 1986-286213/44.
DR   N-PSDB; N60080.
XX
PT   Hepatitis A virus nucleotide sequence and polypeptide - and use
PT   in prodn. of vaccines and diagnostic probes
XX
PS   Claim 5; Fig 1; 18pp; English.
XX
CC   N60080 and oligonucleotide fragments are useful in detection of
CC   hepatitis A virus; transformed hosts may be used for expression of
CC   polypeptides and fragments useful in vaccines without risk of
CC   infection by the virus or in prodn. of particles which are capable
CC   of inducing immmunocompetent B cells for passive immunotherapy. Pref.
CC   epitope is derived from AAs 445-657 or 792-848 of the HAV
CC   polypeptide sequence (P60066).
XX
SQ   Sequence   2227 AA;
```

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Db     799 pykelrlqvgkqrlkyaqee 818
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XX
AC   R15629;
XX
DT   17-MAR-1992  (first entry)
XX
DE   Capsid region of cyno-HAV isolate CY-145.
XX
KW   Hepatitis A virus; cynomolgus; HAV; monkey; vaccine; macaque.
XX
OS   Cynomolgus monkey hepatitis A virus, isolate CY-145.
XX
FH   Key             Location/Qualifiers
FT   Protein         1..245
FT                   /label= VP0
FT   Protein         246..491
FT                   /label= VP3
FT   Protein         492..791
FT                   /label= VP1
FT   Protein         792
FT                   /label= P2
FT                   /note= "incomplete"
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FT   Cleavage-site   491..492
FT   Cleavage-site   791..792
FT   Active-site     315
FT   Active-site     593
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PN   US7678828-A.
XX
PD   12-NOV-1991.
XX
PF   03-APR-1991;   91US-0678828.
XX
PR   03-APR-1991;   91US-0678828.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN.
XX
PI   Hainan OV,  Margolis HS,  Robertson BH,  Brinton MH,  Ebert JW;
XX
DR   WPI; 1991-376737/51.
DR   N-PSDB; Q15180.
XX
PT   Hepatitis A virus isolates and DNA - used to prepare vaccines for
PT   preventing hepatitis A virus infection.
XX
PS   Disclosure; Fig 3; 23pp; English.
XX
CC   The sequence was deduced from the nucleotide sequence obtd. by PCR
CC   amplification of cyno-HAV viral RNA obtd. from the stool of a
CC   cynomolgus monkey with serologically and histologically confirmed
CC   spontaneous hepatitis A. The sequence differs from the  human HAV
CC   isolate HM175 (Cohen, J.I., et al. (1987) Proc. Natl. Acad. Sci.
CC   USA 84, 2497-2501), mainly in the VP3 and VP1 proteins. The Gln-Val
CC   pair at the VP3-VP1 cleavage site in the human isolate is replaced
CC   by a Gln-Thr pair in the cyno-HAV.The other two cleavage sites are
CC   the same.  Two residues have been identified as part of the immuno-
CC   dominant region (see feature table) and are different to those in
CC   the same position in human HAV. The protein and peptides derived
CC   from it can be used in the prepn. of vaccines for the prevention of
CC   HAV infection.
CC   See also R15056.
XX
SQ   Sequence   839 AA;
```

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Qy       1 PYKELRLEVGKQRLKYAQEE 20
           |||||||||||| |||:||
Db     798 pykelrlevgkqrfkyaree 817
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RESULT 15
W42922
ID W42922 standard; peptide; 20 AA.
XX
AC W42922;
XX
DT 28-APR-1998 (first entry)
XX
DE Immunogenic Hepatitis A virus peptide YK-1315.
XX
KW Immunogenic peptide; immunogenic epitope; P2A protein;
KW immune response; antibody.
XX
OS Synthetic.
OS Hepatitis A virus.
XX
PN WO9740147-A1.
XX
PD 30-OCT-1997.
XX
PF 18-APR-1997; 97WO-US06891.
XX
PR 19-APR-1996; 96US-0015644.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Fields HA, Khudyakov YE;
XX
DR WPI; 1997-535831/49.
XX
PT Immunogenic Hepatitis A Virus (HAV) peptide(s) - used to induce an
PT immune response to HAV in a mammal or to detect the presence of
PT antibodies against HAV in a mammal
XX
PS Claim 18; Page 112; 140pp; English.
XX
CC Peptides W42922-30 are immunogenic peptides corresponding to immunogenic
CC epitopes of the Hepatitis A virus (HAV). The peptides are substantially
CC similar to a portion of the amino acid sequence of the P2A protein of HAV
CC corresponding to amino acids 792-980. The present peptide is derived
CC from amino acids 792-811, and has a reactivity of 54.2% with acute sera.
CC Compositions containing the peptides can be used to induce an immune
CC response to HAV in a mammal. The peptides can also be used to detect the
CC presence of antibodies against HAV in mammalian serum. The peptides can
CC also be used to make an antibody against HAV by administering the peptide
CC to a mammal.
XX
SQ Sequence 20 AA;

Query Match 65.7%; Score 67; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      8 pykelrlevgkqr 20
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2001, 16:34:58 ; Search time 62.1 Seconds
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Title: US-09-171-432A-40
Perfect score: 102
Sequence: 1 PYKELRLEVGKQRLKYAQEE 20

Scoring table: BLOSUM62
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Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	102	100.0	1091	6	5516630-2	Patent No. 5516630
2	102	100.0	2227	4	US-08-475-886-2	Sequence 2, Appli
3	102	100.0	2227	4	US-08-475-886-4	Sequence 4, Appli
4	102	100.0	2227	4	US-08-475-886-6	Sequence 6, Appli
5	102	100.0	2227	4	US-08-397-232-2	Sequence 2, Appli
6	102	100.0	2227	4	US-08-397-232-4	Sequence 4, Appli
7	94	92.2	839	1	US-08-087-016-2	Sequence 2, Appli
8	41	40.2	68	1	US-08-606-789-2	Sequence 2, Appli
9	41	40.2	68	1	US-08-606-789-4	Sequence 4, Appli
10	41	40.2	68	2	US-09-111-348-2	Sequence 2, Appli
11	41	40.2	68	2	US-09-111-348-4	Sequence 4, Appli
12	41	40.2	69	5	PCT-US95-06406A-5	Sequence 5, Appli
13	41	40.2	69	5	PCT-US95-06406A-7	Sequence 7, Appli
14	41	40.2	147	1	US-08-264-003B-2	Sequence 2, Appli
15	41	40.2	147	2	US-08-959-865-3	Sequence 3, Appli
16	41	40.2	147	4	US-08-842-234-2	Sequence 2, Appli
17	40	39.2	1463	1	US-08-157-005-3	Sequence 3, Appli
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19	39	38.2	1408	1	US-08-612-521-2	Sequence 2, Appli
20	39	38.2	1898	1	US-08-056-200-94	Sequence 94, Appl
21	39	38.2	1898	2	US-08-800-644-94	Sequence 94, Appl
22	38.5	37.7	641	4	US-08-961-083-160	Sequence 160, App
23	38	37.3	233	3	US-08-836-236-8	Sequence 8, Appli
24	38	37.3	256	2	US-08-719-758-2	Sequence 2, Appli
25	38	37.3	256	4	US-09-119-827-2	Sequence 2, Appli
26	37.5	36.8	18	3	US-08-940-095-229	Sequence 229, App
27	37.5	36.8	18	3	US-08-940-093-229	Sequence 229, App
28	37.5	36.8	18	3	US-08-940-096-229	Sequence 229, App
29	37	36.3	67	3	US-09-120-365-93	Sequence 93, Appl
30	37	36.3	68	1	US-08-606-789-8	Sequence 8, Appli
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32	37	36.3	69	5	PCT-US95-06406A-6	Sequence 6, Appli
33	37	36.3	284	2	US-08-766-439-32	Sequence 32, Appl
34	37	36.3	284	2	US-08-766-439-41	Sequence 41, Appl
35	37	36.3	284	2	US-08-766-439-42	Sequence 42, Appl
36	37	36.3	284	2	US-08-766-439-43	Sequence 43, Appl
37	37	36.3	284	2	US-08-766-439-44	Sequence 44, Appl
38	37	36.3	284	2	US-08-766-439-45	Sequence 45, Appl
39	37	36.3	458	1	US-08-336-618-24	Sequence 24, Appl
40	37	36.3	552	3	US-09-120-365-5	Sequence 5, Appli
41	37	36.3	599	3	US-08-556-419-22	Sequence 22, Appl
42	37	36.3	629	3	US-08-556-419-23	Sequence 23, Appl
43	37	36.3	637	2	US-08-426-125-10	Sequence 10, Appl
44	37	36.3	637	2	US-08-455-355-10	Sequence 10, Appl
45	37	36.3	1091	3	US-08-633-768A-2	Sequence 2, Appli

ALIGNMENTS

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5516630-2
;Patent No. 5516630
;    APPLICANT: TICEHURST, JOHN R.;BALTIMORE, DAVID;FEINSTONE,
;STEPHEN M.;PURCELL, ROBERT H.;RACANIELLO, VINCENT R.;
;BAROUDY, BAHIGE M.
;    TITLE OF INVENTION: METHODS OF DETECTING HEPATITIS A VIRUS
;    NUMBER OF SEQUENCES: 4
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/788,262
;      FILING DATE: 06-NOV-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 256,135
;      FILING DATE: 06-OCT-1988
;      APPLICATION NUMBER: 654,942
;      FILING DATE: 27-SEP-1984
;      APPLICATION NUMBER: 537,911
;      FILING DATE: 30-SEP-1983
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5516630-2


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; Sequence 2, Application US/08475886A
; Patent No. 6113912
; GENERAL INFORMATION:
;  APPLICANT: FUNKHOUSER, ANN W
;  APPLICANT: EMERSON, SUZANNE U
;  APPLICANT: PURCELL, ROBERT H
;  APPLICANT: D'HONDT, ERIC
;  TITLE OF INVENTION: HEPATITIS A VIRUS VACCINES
;  FILE REFERENCE: 20264262US2
;  CURRENT APPLICATION NUMBER: US/08/475,886A
;  CURRENT FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 07/947,338
;  EARLIER FILING DATE: 1992-09-18
;  EARLIER APPLICATION NUMBER: 08/397,232
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;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
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;   ORGANISM: WILD-TYPE HUMAN HEPATITIS A VIRUS, STRAIN HM-175
US-08-475-886-2


  Query Match             100.0%;  Score 102;  DB 4;  Length 2227;
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Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
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RESULT   3
US-08-475-886-4
; Sequence 4, Application US/08475886A
; Patent No. 6113912
; GENERAL INFORMATION:
;  APPLICANT: FUNKHOUSER, ANN W
;  APPLICANT: EMERSON, SUZANNE U
;  APPLICANT: PURCELL, ROBERT H
;  APPLICANT: D'HONDT, ERIC
;  TITLE OF INVENTION: HEPATITIS A VIRUS VACCINES
;  FILE REFERENCE: 20264262US2
;  CURRENT APPLICATION NUMBER: US/08/475,886A
;  CURRENT FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 07/947,338
;  EARLIER FILING DATE: 1992-09-18
;  EARLIER APPLICATION NUMBER: 08/397,232
;  EARLIER FILING DATE: 1995-03-10
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 2227
;   TYPE: PRT
;   ORGANISM: Attenuated HAV (Pass 35), strain HM-175
US-08-475-886-4


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Qy      1 PYKELRLEVGKQRLKYAQEE 20
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Db    799 PYKELRLEVGKQRLKYAQEE 818


RESULT   4
US-08-475-886-6
; Sequence 6, Application US/08475886A
; Patent No. 6113912
; GENERAL INFORMATION:
;  APPLICANT: FUNKHOUSER, ANN W
;  APPLICANT: EMERSON, SUZANNE U
;  APPLICANT: PURCELL, ROBERT H
;  APPLICANT: D'HONDT, ERIC
;  TITLE OF INVENTION: HEPATITIS A VIRUS VACCINES
;  FILE REFERENCE: 20264262US2
;  CURRENT APPLICATION NUMBER: US/08/475,886A
;  CURRENT FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 07/947,338
;  EARLIER FILING DATE: 1992-09-18
;  EARLIER APPLICATION NUMBER: 08/397,232
;  EARLIER FILING DATE: 1995-03-10
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 2227
;   TYPE: PRT
;   ORGANISM: Attenuated (4380) HAV, strain HM-175
US-08-475-886-6


  Query Match             100.0%;  Score 102;  DB 4;  Length 2227;
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Qy      1 PYKELRLEVGKQRLKYAQEE 20
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RESULT   5
US-08-397-232-2
; Sequence 2, Application US/08397232A
; Patent No. 6180110
; GENERAL INFORMATION:
;  APPLICANT: FUNKHOUSER, ANN W
;  APPLICANT: EMERSON, SUZANNE U
;  APPLICANT: PURCELL, ROBERT H
;  APPLICANT: D'HONDT, ERIC
;  TITLE OF INVENTION: HEPATITIS A VIRUS VACCINES
;  FILE REFERENCE: 20264262US1
;  CURRENT APPLICATION NUMBER: US/08/397,232A
;  CURRENT FILING DATE: 1995-04-17
;  EARLIER APPLICATION NUMBER: 07/947,338
;  EARLIER FILING DATE: 1992-09-18
;  EARLIER APPLICATION NUMBER: PCT/US93/08610
;  EARLIER FILING DATE: 1993-09-17
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 2227
;   TYPE: PRT
;   ORGANISM: WILD-TYPE HUMAN HEPATITIS A VIRUS, STRAIN HM-175
US-08-397-232-2


  Query Match             100.0%;  Score 102;  DB 4;  Length 2227;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-08;
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Qy      1 PYKELRLEVGKQRLKYAQEE 20
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Db    799 PYKELRLEVGKQRLKYAQEE 818


RESULT   6
US-08-397-232-4
; Sequence 4, Application US/08397232A
; Patent No. 6180110
; GENERAL INFORMATION:
;  APPLICANT: FUNKHOUSER, ANN W
;  APPLICANT: EMERSON, SUZANNE U
;  APPLICANT: PURCELL, ROBERT H
;  APPLICANT: D'HONDT, ERIC
;  TITLE OF INVENTION: HEPATITIS A VIRUS VACCINES
;  FILE REFERENCE: 20264262US1
;  CURRENT APPLICATION NUMBER: US/08/397,232A
;  CURRENT FILING DATE: 1995-04-17
;  EARLIER APPLICATION NUMBER: 07/947,338
;  EARLIER FILING DATE: 1992-09-18
;  EARLIER APPLICATION NUMBER: PCT/US93/08610
;  EARLIER FILING DATE: 1993-09-17
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 2227
;   TYPE: PRT
;   ORGANISM: Attenuated (4380) HAV, strain HM-175
US-08-397-232-4
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  Query Match           100.0%;  Score 102;  DB 4;  Length 2227;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-08;
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Qy      1 PYKELRLEVGKQRLKYAQEE 20
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Db    799 PYKELRLEVGKQRLKYAQEE 818


RESULT   7
US-08-087-016-2
; Sequence 2, Application US/08087016
; Patent No. 5430135
;  GENERAL INFORMATION:
;    APPLICANT:  NAINAN, OMANA V.
;    APPLICANT:  MARGOLIS, HAROLD S.
;    APPLICANT:  ROBERTSON, BETTY H.
;    APPLICANT:  BRINTON, MARGO H.
;    APPLICANT:  EBERT, JAMES W.
;    TITLE OF INVENTION:  HEPATITIS A VIRUS VACCINE
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CUSHMAN, DARBY & CUSHMAN
;      STREET:  1615 L Street N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/087,016
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/678,828
;      FILING DATE:  03-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SCOTT, WATSON T.
;      REGISTRATION NUMBER:  26,581
;      REFERENCE/DOCKET NUMBER:  WTS/5683/83834/SRL
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 861-3000
;      TELEFAX:  (202) 822-0944
;      TELEX:  6714627 CUSH
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  839 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-087-016-2


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Qy      1 PYKELRLEVGKQRLKYAQEE 20
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Db    798 PYKELRLEVGKQRFKYAREE 817


RESULT   8
US-08-606-789-2
; Sequence 2, Application US/08606789
; Patent No. 5783418
;  GENERAL INFORMATION:
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Murry, Lynn E.
;    APPLICANT:  Guegler, Kark J.
;    APPLICANT:  Seilhamer, Jeffrey J.
;    TITLE OF INVENTION:  HUMAN HOMOLOG OF THE RAT G PROTEIN
;    TITLE OF INVENTION:  GAMMA-5 SUBUNIT
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/606,789
;      FILING DATE:  Filed Herewith
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/440,743
;      FILING DATE:  May 5, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/320,011
;      FILING DATE:  October 5, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Luther, Barbara J.
;      REGISTRATION NUMBER:  33,954
;      REFERENCE/DOCKET NUMBER:  PF-0055 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-852-0195
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  68 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  PITUITARY
;      CLONE:  112530
US-08-606-789-2


  Query Match           40.2%;  Score 41;  DB 1;  Length 68;
  Best Local Similarity  50.0%;  Pred. No. 4.6;
  Matches    8;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      3 KELRLEVGKQRLKYAQ 18
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Db     15 QQLRLEAGLNRVKVSQ 30


RESULT   9
US-08-606-789-4
; Sequence 4, Application US/08606789
; Patent No. 5783418
;  GENERAL INFORMATION:
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Murry, Lynn E.
;    APPLICANT:  Guegler, Kark J.
;    APPLICANT:  Seilhamer, Jeffrey J.
;    TITLE OF INVENTION:  HUMAN HOMOLOG OF THE RAT G PROTEIN
;    TITLE OF INVENTION:  GAMMA-5 SUBUNIT
;    NUMBER OF SEQUENCES:  31
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;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/606,789
;      FILING DATE:  Filed Herewith
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/440,743
;      FILING DATE:  May 5, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/320,011
;      FILING DATE:  October 5, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Luther, Barbara J.
;      REGISTRATION NUMBER:  33,954
;      REFERENCE/DOCKET NUMBER:  PF-0055 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-852-0195
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  68 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  204241
US-08-606-789-4


  Query Match             40.2%;  Score 41;  DB 1;  Length 68;
  Best Local Similarity   50.0%;  Pred. No. 4.6;
  Matches    8;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3 KELRLEVGKQRLKYAQ 18
           ::|||| |  |:| :|
Db      15 QQLRLEAGLNRVKVSQ 30


RESULT  10
US-09-111-348-2
; Sequence 2, Application US/09111348
; Patent No. 5912130
;  GENERAL INFORMATION:
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Murry, Lynn E.
;    APPLICANT:  Guegler, Kark J.
;    APPLICANT:  Seilhamer, Jeffrey J.
;    TITLE OF INVENTION:  HUMAN HOMOLOG OF THE RAT G PROTEIN
;    TITLE OF INVENTION:  GAMMA-5 SUBUNIT
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/111,348
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/606,789
;      FILING DATE:
;      APPLICATION NUMBER:  08/440,743
;      FILING DATE:  May 5, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/320,011
;      FILING DATE:  October 5, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Luther, Barbara J.
;      REGISTRATION NUMBER:  33,954
;      REFERENCE/DOCKET NUMBER:  PF-0055 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-852-0195
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  68 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  PITUITARY
;      CLONE:  112530
US-09-111-348-2


  Query Match             40.2%;  Score 41;  DB 2;  Length 68;
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  Matches    8;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3 KELRLEVGKQRLKYAQ 18
           ::|||| |  |:| :|
Db      15 QQLRLEAGLNRVKVSQ 30


RESULT  11
US-09-111-348-4
; Sequence 4, Application US/09111348
; Patent No. 5912130
;  GENERAL INFORMATION:
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Murry, Lynn E.
;    APPLICANT:  Guegler, Kark J.
;    APPLICANT:  Seilhamer, Jeffrey J.
;    TITLE OF INVENTION:  HUMAN HOMOLOG OF THE RAT G PROTEIN
;    TITLE OF INVENTION:  GAMMA-5 SUBUNIT
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/111,348
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;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/606,789
;       FILING DATE:
;       APPLICATION NUMBER:  08/440,743
;       FILING DATE:  May 5, 1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/320,011
;       FILING DATE:  October 5, 1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Luther, Barbara J.
;       REGISTRATION NUMBER:  33,954
;       REFERENCE/DOCKET NUMBER:  PF-0055 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-855-0555
;       TELEFAX:  415-852-0195
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  68 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     IMMEDIATE SOURCE:
;       LIBRARY:  GenBank
;       CLONE:  204241
US-09-111-348-4


  Query Match             40.2%;  Score 41;  DB 2;  Length 68;
  Best Local Similarity   50.0%;  Pred. No. 4.6;
  Matches    8;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3 KELRLEVGKQRLKYAQ 18
           ::|||| |  |:| :|
Db      15 QQLRLEAGLNRVKVSQ 30


RESULT  12
PCT-US95-06406A-5
; Sequence 5, Application PC/TUS9506406A
;  GENERAL INFORMATION:
;    APPLICANT:  Janet D. Robishaw, Charles Kunsch
;    TITLE OF INVENTION:  cDNA Clones Encoding Human G Protein
;    TITLE OF INVENTION:  Subunits
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:
;      STREET:
;      CITY:
;      STATE:
;      COUNTRY:
;      ZIP:
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;      COMPUTER:  IBM 486
;      OPERATING SYSTEM:  WINDOWS FOR WORKGROUPS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06406A
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:
;      REGISTRATION NUMBER:
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:
;      TELEFAX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  69
;      TYPE:  AMINO ACID
;      TOPOLOGY:  LINEAR
PCT-US95-06406A-5


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  Best Local Similarity   50.0%;  Pred. No. 4.7;
  Matches    8;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3 KELRLEVGKQRLKYAQ 18
           ::|||| |  |:| :|
Db      15 QQLRLEAGLNRVKVSQ 30


RESULT  13
PCT-US95-06406A-7
; Sequence 7, Application PC/TUS9506406A
;  GENERAL INFORMATION:
;    APPLICANT:  Janet D. Robishaw, Charles Kunsch
;    TITLE OF INVENTION:  cDNA Clones Encoding Human G Protein
;    TITLE OF INVENTION:  Subunits
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:
;      STREET:
;      CITY:
;      STATE:
;      COUNTRY:
;      ZIP:
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;      COMPUTER:  IBM 486
;      OPERATING SYSTEM:  WINDOWS FOR WORKGROUPS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06406A
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:
;      REGISTRATION NUMBER:
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:
;      TELEFAX:
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  69
;      TYPE:  AMINO ACID
;      TOPOLOGY:  LINEAR
PCT-US95-06406A-7


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Qy       3 KELRLEVGKQRLKYAQ 18
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Db      15 EQLKLEAGVERIKVSQ 30


RESULT  14
US-08-264-003B-2
; Sequence 2, Application US/08264003B
; Patent No. 5696076
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;  GENERAL INFORMATION:
;    APPLICANT:  Gentz, Reiner
;    APPLICANT:  Fleischmann, Robert D.
;    TITLE OF INVENTION:  5-LIPOXYGENASE-ACTIVATING PROTEIN II
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
;      ADDRESSEE:  STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/264,003B
;      FILING DATE:  06-JUN-1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ferraro, Gregory D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  147 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-264-003B-2


  Query Match             40.2%;  Score 41;  DB 1;  Length 147;
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Db      24 LQVGKARLKY 33


RESULT  15
US-08-959-865-3
; Sequence 3, Application US/08959865
; Patent No. 5919627
;  GENERAL INFORMATION:
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Corley, Neil C.
;    APPLICANT:  Shah, Purvi
;    TITLE OF INVENTION:  MICROSOMAL GLUTATHIONE-S TRANSFERASE
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,865
;      FILING DATE:  Herewith
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0411 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  147 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  COLNNOT07
;      CLONE:  903729
US-08-959-865-3


  Query Match             40.2%;  Score 41;  DB 2;  Length 147;
  Best Local Similarity   80.0%;  Pred. No. 10;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       7 LEVGKQRLKY 16
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Db      24 LQVGKARLKY 33


Search completed: April 24, 2001, 16:34:59
Job time: 530 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2001, 16:25:42 ; Search time 73.14 Seconds
(without alignments)
18.792 Million cell updates/sec

Title: US-09-171-432A-40
Perfect score: 102
Sequence: 1 PYKELRLEVGKQRLKYAQEE 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_67:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	102	100.0	55	2	PQ0433	genome polyprotein
2	102	100.0	56	2	PQ0434	genome polyprotein
3	102	100.0	56	2	PQ0428	genome polyprotein
4	102	100.0	56	2	PQ0432	genome polyprotein
5	102	100.0	56	2	PQ0430	genome polyprotein
6	102	100.0	341	2	S04137	genome polyprotein
7	102	100.0	852	1	GNNYHA	genome polyprotein
8	102	100.0	1358	2	A03905	genome polyprotein
9	102	100.0	2227	1	GNNYHM	genome polyprotein
10	102	100.0	2227	1	GNNYHR	genome polyprotein
11	102	100.0	2227	1	GNNYMK	genome polyprotein
12	102	100.0	2227	1	GNNYHB	genome polyprotein
13	100	98.0	56	2	PQ0427	genome polyprotein
14	99	97.1	56	2	PQ0429	genome polyprotein
15	95	93.1	56	2	PQ0436	genome polyprotein
16	95	93.1	2230	1	GNNYSA	genome polyprotein
17	94	92.2	55	2	PQ0435	genome polyprotein
18	94	92.2	56	2	PQ0437	genome polyprotein
19	94	92.2	839	1	GNNYS2	genome polyprotein
20	93	91.2	56	2	PQ0431	genome polyprotein
21	62	60.8	319	2	JH0135	genome polyprotein
22	46	45.1	219	2	T45997	hypothetical prote
23	46	45.1	285	2	T29804	hypothetical prote
24	45	44.1	209	2	D72121	ATP synthase chain
25	44	43.1	290	2	C71701	branched-chain ami
26	44	43.1	776	2	T09938	hypothetical prote
27	43	42.2	208	1	F70485	uracil phosphoribo
28	43	42.2	465	2	T25441	hypothetical prote
29	43	42.2	509	2	G81929	probable iron-upta
30	43	42.2	534	2	JC5096	transposase - fung
31	43	42.2	3587	2	T31075	tyrocidine synthet
32	42.5	41.7	179	2	A65027	hypothetical prote
33	42	41.2	452	2	B83623	probable porin PA0
34	42	41.2	736	2	B82944	ribose/galactose A
35	42	41.2	752	2	A65089	DNA topoisomerase
36	42	41.2	752	2	A45582	DNA topoisomerase
37	42	41.2	939	2	H71532	valine--tRNA ligas
38	42	41.2	4131	2	T21085	hypothetical prote
39	41	40.2	68	2	B42243	GTP-binding regula
40	41	40.2	68	2	I39158	GTP-binding regula
41	41	40.2	151	2	A72409	conserved hypothet
42	41	40.2	412	2	E70108	aminopeptidase II
43	41	40.2	446	2	G70774	probable atpH prot
44	41	40.2	515	2	H75579	hypothetical prote
45	41	40.2	656	2	E75468	hypothetical prote

ALIGNMENTS

RESULT 1
PQ0433
genome polyprotein - human hepatitis A virus (strain PA21) (fragment)
C;Species: human hepatitis A virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PQ0433
R;Robertson, B.H.; Jansen, R.W.; Khanna, B.; Totsuka, A.; Nainan, O.V.; Siegl, G.; Wi
J. Gen. Virol. 73, 1365-1377, 1992
A;Title: Genetic relatedness of hepatitis A virus strains recovered from different ge
A;Reference number: PQ0427; MUID:92300330
A;Accession: PQ0433
A;Molecule type: mRNA
A;Residues: 1-55 <ROB>
A;Note: this protein is from the VP1/2A Junction region
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; polyprotein

Query Match 100.0%; Score 102; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 PYKELRLEVGKQRLKYAQEE 20
           ||||||||||||||||||||
Db      35 PYKELRLEVGKQRLKYAQEE 54
```

RESULT 2
PQ0434
genome polyprotein - human hepatitis A virus (strain KPH) (fragment)
C;Species: human hepatitis A virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PQ0434
R;Robertson, B.H.; Jansen, R.W.; Khanna, B.; Totsuka, A.; Nainan, O.V.; Siegl, G.; Wi
J. Gen. Virol. 73, 1365-1377, 1992
A;Title: Genetic relatedness of hepatitis A virus strains recovered from different ge
A;Reference number: PQ0427; MUID:92300330
A;Accession: PQ0434
A;Molecule type: mRNA
A;Residues: 1-56 <ROB>
A;Note: this protein is from the VP1/2A Junction region
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; polyprotein

Query Match 100.0%; Score 102; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 PYKELRLEVGKQRLKYAQEE 20
           ||||||||||||||||||||
Db      36 PYKELRLEVGKQRLKYAQEE 55
```

RESULT 3
PQ0428
genome polyprotein - human hepatitis A virus (strain TKM002) (fragment)
C;Species: human hepatitis A virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PQ0428
R;Robertson, B.H.; Jansen, R.W.; Khanna, B.; Totsuka, A.; Nainan, O.V.; Siegl, G.; Widel
J. Gen. Virol. 73, 1365-1377, 1992
A;Title: Genetic relatedness of hepatitis A virus strains recovered from different geogr
A;Reference number: PQ0427; MUID:92300330
A;Accession: PQ0428
A;Molecule type: mRNA
A;Residues: 1-56 <ROB>
A;Note: this protein is from the VP1/2A Junction region
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; polyprotein

Query Match 100.0%; Score 102; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYKELRLEVGKQRLKYAQEE 20
||||||||||||||||||||
Db 36 PYKELRLEVGKQRLKYAQEE 55

RESULT 4
PQ0432
genome polyprotein - human hepatitis A virus (strain CF-53) (fragment)
C;Species: human hepatitis A virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PQ0432
R;Robertson, B.H.; Jansen, R.W.; Khanna, B.; Totsuka, A.; Nainan, O.V.; Siegl, G.; Widel
J. Gen. Virol. 73, 1365-1377, 1992
A;Title: Genetic relatedness of hepatitis A virus strains recovered from different geogr
A;Reference number: PQ0427; MUID:92300330
A;Accession: PQ0432
A;Molecule type: mRNA
A;Residues: 1-56 <ROB>
A;Note: this protein is from the VP1/2A Junction region
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; polyprotein

Query Match 100.0%; Score 102; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYKELRLEVGKQRLKYAQEE 20
||||||||||||||||||||
Db 36 PYKELRLEVGKQRLKYAQEE 55

RESULT 5
PQ0430
genome polyprotein - human hepatitis A virus (strain S23-1) (fragment)
C;Species: human hepatitis A virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PQ0430
R;Robertson, B.H.; Jansen, R.W.; Khanna, B.; Totsuka, A.; Nainan, O.V.; Siegl, G.; Widel
J. Gen. Virol. 73, 1365-1377, 1992
A;Title: Genetic relatedness of hepatitis A virus strains recovered from different geogr
A;Reference number: PQ0427; MUID:92300330
A;Accession: PQ0430
A;Molecule type: mRNA
A;Residues: 1-56 <ROB>
A;Note: this protein is from the VP1/2A Junction region
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; polyprotein

Query Match 100.0%; Score 102; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYKELRLEVGKQRLKYAQEE 20
||||||||||||||||||||
Db 36 PYKELRLEVGKQRLKYAQEE 55

RESULT 6
S04137
genome polyprotein - human hepatitis A virus (strain LCDC-1) (fragment)
C;Species: human hepatitis A virus
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 21-Jul-2000
C;Accession: S04137
R;Andonov, A.P.; Lau, P.C.K.; Chaudhary, R.
Nucleic Acids Res. 17, 3594, 1989
A;Title: Nucleotide sequence of the VP1 gene from a Chinese strain of hepatitis A vir
A;Reference number: S04137; MUID:89263805
A;Accession: S04137
A;Molecule type: mRNA
A;Residues: 1-341 <AND>
A;Cross-references: EMBL:X14666; NID:g62301; PIDN:CAA32794.1; PID:g4377576
C;Genetics:
A;Gene: VP1
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; polyprotein
F;2-340/Product: coat protein 1D (VP1) #status predicted <MAT>

Query Match 100.0%; Score 102; DB 2; Length 341;
Best Local Similarity 100.0%; Pred. No. 9.8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYKELRLEVGKQRLKYAQEE 20
||||||||||||||||||||
Db 303 PYKELRLEVGKQRLKYAQEE 322

RESULT 7
GNNYHA
genome polyprotein - human hepatitis A virus (strain CR326) (fragment)
N;Contains: coat protein 1A; coat protein 1B; coat protein 1C; core protein 2A
C;Species: human hepatitis A virus
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
C;Accession: A03904
R;Linemeyer, D.L.; Menke, J.G.; Martin-Gallardo, A.; Hughes, J.V.; Young, A.; Mitra,
J. Virol. 54, 247-255, 1985
A;Title: Molecular cloning and partial sequencing of hepatitis A viral cDNA.
A;Reference number: A03904; MUID:85185648
A;Accession: A03904
A;Molecule type: genomic RNA
A;Residues: 1-852 <LIN>
A;Cross-references: EMBL:M10033; NID:g329592; PIDN:AAA45470.1; PID:g329593
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; polyprotein
F;1-245/Product: coat protein 1A #status predicted <C1A>
F;246-491/Product: coat protein 1B #status predicted <C1B>
F;492-836/Product: coat protein 1C #status predicted <C1C>
F;837-852/Product: core protein 2A (fragment) #status predicted <C2A>

Query Match 100.0%; Score 102; DB 1; Length 852;
Best Local Similarity 100.0%; Pred. No. 2.7e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYKELRLEVGKQRLKYAQEE 20
||||||||||||||||||||
Db 799 PYKELRLEVGKQRLKYAQEE 818

```
RESULT   8
A03905
genome polyprotein (version 2) - human hepatitis A virus (fragments)
N;Contains: coat protein 1A; coat protein 1B; coat protein 1C; core protein 2A; protein
C;Species: human hepatitis A virus
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 15-Nov-1996
C;Accession: A03905
R;Baroudy, B.M.; Ticehurst, J.R.; Miele, T.A.; Maizel Jr., J.V.; Purcell, R.H.; Feinstor
Proc. Natl. Acad. Sci. U.S.A. 82, 2143-2147, 1985
A;Title: Sequence analysis of hepatitis A virus cDNA coding for capsid proteins and RNA
A;Reference number: A03905; MUID:85166289
A;Accession: A03905
A;Molecule type: genomic RNA
A;Residues: 1-1358 <BAR>
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; polyprotein
F;1-245/Product: coat protein 1A #status predicted <C1A>
F;246-491/Product: coat protein 1B #status predicted <C1B>
F;492-836/Product: coat protein 1C #status predicted <C1C>
F;837-854/Product: core protein 2A (fragment) #status predicted <C2A>
F;855-1358/Product: protein 3D (RNA polymerase) (fragment) #status predicted <C3D>


  Query Match             100.0%;  Score 102;  DB 2;  Length 1358;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 PYKELRLEVGKQRLKYAQEE 20
           ||||||||||||||||||||
Db     799 PYKELRLEVGKQRLKYAQEE 818


RESULT   9
GNNYHM
genome polyprotein - human hepatitis A virus (strain HM-175, wild type)
N;Contains: coat protein 1A; coat protein 1B; coat protein 1C; coat protein 1D; core pro
B; RNA-directed RNA polymerase (EC 2.7.7.48), protein 3D
C;Species: human hepatitis A virus
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jul-1999
C;Accession: A25981
R;Cohen, J.I.; Ticehurst, J.R.; Purcell, R.H.; Buckler-White, A.; Baroudy, B.M.
J. Virol. 61, 50-59, 1987
A;Title: Complete nucleotide sequence of wild-type hepatitis A virus: comparison with di
A;Reference number: A25981; MUID:87061253
A;Accession: A25981
A;Molecule type: genomic RNA
A;Residues: 1-2227 <COH>
A;Cross-references: EMBL:M14707; NID:g329582; PIDN:AAA45465.1; PID:g329583
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; cysteine proteinase; hydrolase; nucleotidyltrans
F;1-23/Product: coat protein 1A #status predicted <VP4>
F;24-245/Product: coat protein 1B #status predicted <VP2>
F;246-491/Product: coat protein 1C #status predicted <VP3>
F;492-791/Product: coat protein 1D #status predicted <VP1>
F;792-980/Product: core protein 2A #status predicted <C2A>
F;981-1087/Product: core protein 2B #status predicted <C2B>
F;1088-1422/Product: core protein 2C #status predicted <C2C>
F;1423-1496/Product: protein 3A #status predicted <C3A>
F;1497-1519/Product: protein 3B #status predicted <C3B>
F;1520-1738/Product: cysteine proteinase, protein 3C #status predicted <C3C>
F;1739-2227/Product: RNA-directed RNA polymerase, protein 3D #status predicted <C3D>


  Query Match             100.0%;  Score 102;  DB 1;  Length 2227;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 PYKELRLEVGKQRLKYAQEE 20
           ||||||||||||||||||||
Db     799 PYKELRLEVGKQRLKYAQEE 818


RESULT  10
GNNYHR
genome polyprotein - human hepatitis A virus
N;Contains: coat protein 1A; coat protein 1B; coat protein 1C; core protein 2A; core
NA polymerase (EC 2.7.7.48), protein 3D
C;Species: human hepatitis A virus
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
C;Accession: A03903
R;Najarian, R.; Caput, D.; Gee, W.; Potter, S.J.; Renard, A.; Merryweather, J.; van N
Proc. Natl. Acad. Sci. U.S.A. 82, 2627-2631, 1985
A;Title: Primary structure and gene organization of human hepatitis A virus.
A;Reference number: A03903; MUID:85190549
A;Accession: A03903
A;Molecule type: genomic RNA
A;Residues: 1-2227 <NAJ>
A;Cross-references: GB:K02990; NID:g329596; PIDN:AAA45472.1; PID:g329597
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; cysteine proteinase; hydrolase; nucleotidyltr
F;1-245/Product: coat protein 1A #status predicted <C1A>
F;246-491/Product: coat protein 1B #status predicted <C1B>
F;492-836/Product: coat protein 1C #status predicted <C1C>
F;837-980/Product: core protein 2A #status predicted <C2A>
F;981-1076/Product: core protein 2B #status predicted <C2B>
F;1077-1422/Product: core protein 2C #status predicted <C2C>
F;1423-1484/Product: protein 3A #status predicted <C3A>
F;1485-1507/Product: protein 3B #status predicted <C3B>
F;1508-1678/Product: cysteine proteinase, protein 3C #status predicted <C3C>
F;1679-2227/Product: RNA-directed RNA polymerase, protein 3D #status predicted <C3D>


  Query Match             100.0%;  Score 102;  DB 1;  Length 2227;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 PYKELRLEVGKQRLKYAQEE 20
           ||||||||||||||||||||
Db     799 PYKELRLEVGKQRLKYAQEE 818


RESULT  11
GNNYMK
genome polyprotein - human hepatitis A virus (strain HM-175/7MK-5, attenuated HAV)
N;Contains: coat protein 1A; coat protein 1B; coat protein 1C; core protein 2A; core
NA polymerase (EC 2.7.7.48), protein 3D
C;Species: human hepatitis A virus
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
C;Accession: A94149; A25914; A94508
R;Cohen, J.I.; Rosenblum, B.; Ticehurst, J.R.; Daemer, R.J.; Feinstone, S.M.; Purcell
Proc. Natl. Acad. Sci. U.S.A. 84, 2497-2501, 1987
A;Title: Complete nucleotide sequence of an attenuated hepatitis A virus: comparison
A;Reference number: A94149; MUID:87175701
A;Accession: A94149
A;Status: nucleic acid sequence not shown
A;Molecule type: genomic RNA
A;Residues: 1-2227 <COH>
A;Cross-references: EMBL:M16632; NID:g329594; PIDN:AAA45471.1; PID:g329595
A;Note: submitted to GenBank, August 1987
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; cysteine proteinase; hydrolase; nucleotidyltr
F;1-245/Product: coat protein 1A #status predicted <P1A>
F;246-491/Product: coat protein 1B #status predicted <P1B>
F;492-836/Product: coat protein 1C #status predicted <P1C>
F;837-980/Product: core protein 2A #status predicted <P2A>
F;981-1076/Product: core protein 2B #status predicted <P2B>
F;1077-1422/Product: core protein 2C #status predicted <P2C>
F;1423-1484/Product: protein 3A #status predicted <P3A>
F;1485-1507/Product: protein 3B #status predicted <P3B>
F;1508-1678/Product: cysteine proteinase, protein 3C #status predicted <P3C>
F;1679-2227/Product: RNA-directed RNA polymerase, protein 3D #status predicted <P3D>
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```
  Query Match            100.0%;  Score 102;  DB 1;  Length 2227;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 PYKELRLEVGKQRLKYAQEE 20
           ||||||||||||||||||||
Db     799 PYKELRLEVGKQRLKYAQEE 818


RESULT  12
GNNYHB
genome polyprotein - human hepatitis A virus (strain MBB)
N;Contains: coat protein 1A; coat protein 1B; coat protein 1C; coat protein 1D; core pro
 VPg; protein 3A; RNA-directed RNA polymerase (EC 2.7.7.48), protein 3D
C;Species: human hepatitis A virus
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-May-1996
C;Accession: JS0303
R;Paul, A.V.; Tada, H.; von der Helm, K.; Wissel, T.; Kiehn, R.; Wimmer, E.; Deinhardt,
Virus Res. 8, 153-171, 1987
A;Title: The entire nucleotide sequence of the genome of human hepatitis A virus (isolat
A;Reference number: JS0303; MUID:88045071
A;Accession: JS0303
A;Molecule type: genomic RNA
A;Residues: 1-2227 <PAU>
A;Cross-references: EMBL:M20273
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; cysteine proteinase; genome-linked protein; hydr
F;1-23/Product: coat protein 1A #status predicted <VP4>
F;24-246/Product: coat protein 1B #status predicted <VP2>
F;247-491/Product: coat protein 1C #status predicted <VP3>
F;492-836/Product: coat protein 1D #status predicted <VP1>
F;837-980/Product: core protein 2A #status predicted <P2A>
F;981-1108/Product: core protein 2B #status predicted <P2B>
F;1109-1438/Product: core protein 2C #status predicted <P2C>
F;1439-1496/Product: protein 3A #status predicted <P3A>
F;1497-1519/Product: genome-linked protein VPg #status predicted <VPG>
F;1520-1736/Product: cysteine proteinase, protein 3C #status predicted <P3C>
F;1737-2227/Product: RNA-directed RNA polymerase, protein 3D #status predicted <P3D>


  Query Match            100.0%;  Score 102;  DB 1;  Length 2227;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 PYKELRLEVGKQRLKYAQEE 20
           ||||||||||||||||||||
Db     799 PYKELRLEVGKQRLKYAQEE 818


RESULT  13
PQ0427
genome polyprotein - human hepatitis A virus (strain EP-35.730) (fragment)
C;Species: human hepatitis A virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PQ0427
R;Robertson, B.H.; Jansen, R.W.; Khanna, B.; Totsuka, A.; Nainan, O.V.; Siegl, G.; Widel
J. Gen. Virol. 73, 1365-1377, 1992
A;Title: Genetic relatedness of hepatitis A virus strains recovered from different geogr
A;Reference number: PQ0427; MUID:92300330
A;Accession: PQ0427
A;Molecule type: mRNA
A;Residues: 1-56 <ROB>
C;Comment: This protein is from the VP1/2A Junction region.
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; polyprotein


  Query Match            98.0%;  Score 100;  DB 2;  Length 56;
  Best Local Similarity   95.0%;  Pred. No. 2.8e-09;
  Matches   19;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 PYKELRLEVGKQRLKYAQEE 20
           ||||||:|||||||||||||
Db      36 PYKELRMEVGKQRLKYAQEE 55


RESULT  14
PQ0429
genome polyprotein - human hepatitis A virus (strain PRC16) (fragment)
C;Species: human hepatitis A virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PQ0429
R;Robertson, B.H.; Jansen, R.W.; Khanna, B.; Totsuka, A.; Nainan, O.V.; Siegl, G.; Wi
J. Gen. Virol. 73, 1365-1377, 1992
A;Title: Genetic relatedness of hepatitis A virus strains recovered from different ge
A;Reference number: PQ0427; MUID:92300330
A;Accession: PQ0429
A;Molecule type: mRNA
A;Residues: 1-56 <ROB>
A;Note: this protein is from the VP1/2A Junction region
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; polyprotein


  Query Match            97.1%;  Score 99;  DB 2;  Length 56;
  Best Local Similarity   95.0%;  Pred. No. 4.1e-09;
  Matches   19;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 PYKELRLEVGKQRLKYAQEE 20
           |||:|||||||||||||||
Db      36 PYKDLRLEVGKQRLKYAQEE 55


RESULT  15
PQ0436
genome polyprotein - human hepatitis A virus (strain AGM27) (fragment)
C;Species: human hepatitis A virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PQ0436
R;Robertson, B.H.; Jansen, R.W.; Khanna, B.; Totsuka, A.; Nainan, O.V.; Siegl, G.; Wi
J. Gen. Virol. 73, 1365-1377, 1992
A;Title: Genetic relatedness of hepatitis A virus strains recovered from different ge
A;Reference number: PQ0427; MUID:92300330
A;Accession: PQ0436
A;Molecule type: mRNA
A;Residues: 1-56 <ROB>
A;Note: this protein is from the VP1/2A Junction region
C;Superfamily: hepatitis A virus genome polyprotein
C;Keywords: coat protein; core protein; polyprotein


  Query Match            93.1%;  Score 95;  DB 2;  Length 56;
  Best Local Similarity   90.0%;  Pred. No. 1.8e-08;
  Matches   18;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 PYKELRLEVGKQRLKYAQEE 20
           ||||||:||||||||| ||
Db      36 PYKELRMEVGKQRLKYAMEE 55


Search completed: April 24, 2001, 16:25:46
Job time: 280 sec
```

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2001, 16:33:53 ; Search time 38.74 Seconds
(without alignments)
17.685 Million cell updates/sec

Title: US-09-171-432A-40
Perfect score: 102
Sequence: 1 PYKELRLEVGKQRLKYAQEE 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	102	100.0	341	1	POLG_HPAV1	P13672 hepatitis a
2	102	100.0	808	1	POLG_HPAVG	Q02381 hepatitis a
3	102	100.0	852	1	POLG_HPAVC	P06442 hepatitis a
4	102	100.0	2226	1	POLG_HPAV2	P26580 hepatitis a
5	102	100.0	2226	1	POLG_HPAV4	P26581 hepatitis a
6	102	100.0	2226	1	POLG_HPAV8	P26582 hepatitis a
7	102	100.0	2227	1	POLG_HPAVH	P08617 hepatitis a
8	102	100.0	2227	1	POLG_HPAVL	P06441 hepatitis a
9	102	100.0	2227	1	POLG_HPAVM	P13901 hepatitis a
10	95	93.1	2230	1	POLG_HPAVS	P14553 simian hepa
11	94	92.2	839	1	POLG_HPAVT	P31788 simian hepa
12	45	44.1	209	1	VATD_CHLPN	Q9z991 chlamydia p
13	44	43.1	290	1	ILVE_RICPR	O05970 rickettsia
14	44	43.1	583	1	FOJO_DROME	P54360 drosophila
15	43	42.2	208	1	UPP_AQUAE	O67914 aquifex aeo
16	43	42.2	507	1	DNAA_RHIME	P35890 rhizobium m
17	43	42.2	3587	1	TYCB_BACBR	O30408 b tyrocidin
18	42	41.2	752	1	PARC_ECOLI	P20082 escherichia
19	42	41.2	752	1	PARC_SALTY	P26973 salmonella
20	42	41.2	939	1	SYV_CHLTR	O84304 chlamydia t
21	41	40.2	68	1	GBG5_HUMAN	P30670 homo sapien
22	41	40.2	68	1	GBGA_HUMAN	P50151 homo sapien
23	41	40.2	147	1	GST2_HUMAN	Q99735 homo sapien
24	41	40.2	318	1	YZ34_AQUAE	O66423 aquifex aeo
25	41	40.2	446	1	ATPD_MYCTU	Q10594 mycobacteri
26	40	39.2	69	1	MOP_HAEIN	P45183 haemophilus
27	40	39.2	456	1	EF1A_DICDI	P18624 dictyosteli
28	40	39.2	470	1	BFR1_YEAST	P38934 saccharomyc
29	40	39.2	723	1	SYM_PYRHO	O58721 pyrococcus
30	40	39.2	733	1	ERG7_RAT	P48450 rattus norv
31	40	39.2	764	1	UBF1_HUMAN	P17480 homo sapien
32	40	39.2	764	1	UBF1_RAT	P25977 rattus norv
33	40	39.2	765	1	UBF1_MOUSE	P25976 mus musculu
34	40	39.2	795	1	LON_MYCPN	P78025 mycoplasma
35	40	39.2	939	1	SYV_CHLMU	Q9pk91 chlamydia m
36	40	39.2	3859	1	RPOA_LELV	Q04561 lelystad vi
37	39.5	38.7	971	1	SN2L_CAEEL	P41877 caenorhabdi
38	39.5	38.7	976	1	SN21_HUMAN	P28370 homo sapien
39	39.5	38.7	1812	1	BRC1_MOUSE	P48754 mus musculu
40	39	38.2	46	1	DIUH_LOCMI	P23465 locusta mig
41	39	38.2	362	1	ILVE_STRCO	O86505 streptomyce
42	39	38.2	424	1	EXON_NPVOP	P24081 orgyia pseu
43	39	38.2	508	1	V56K_PLRV1	P17525 potato leaf
44	39	38.2	508	1	V56K_PLRVW	P11626 potato leaf
45	39	38.2	653	1	PABP_SCHPO	P31209 schizosacch

ALIGNMENTS

RESULT 1
POLG_HPAV1
ID P13672; STANDARD; PRT; 341 AA.
AC
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP3; CORE PROTEIN
DE P2A] (FRAGMENT).
OS Hepatitis A virus (strain LCDC-1).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Hepatovirus.
OX NCBI_TaxID=12093;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89263805; PubMed=2542903;
RA Andonov A.P., Lau P., Chaudhary R.;
RT "Nucleotide sequence of the VP1 gene from a Chinese strain of
RT hepatitis A virus (HAV).";
RL Nucleic Acids Res. 17:3594-3594(1989).
CC -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC ---
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CC ---
DR EMBL; X14666; CAA32794.1; -.
DR PIR; S04137; S04137.
KW Polyprotein; Coat protein; Core protein.
FT NON_TER 1 1
FT CHAIN <1 1 COAT PROTEIN VP3 (1C).
FT CHAIN 2 340 COAT PROTEIN VP1 (1D).
FT CHAIN 341 >341 CORE PROTEIN P2A.
FT NON_TER 341 341
SQ SEQUENCE 341 AA; 38003 MW; 066918289BF126D5 CRC64;

Query Match 100.0%; Score 102; DB 1; Length 341;
Best Local Similarity 100.0%; Pred. No. 6.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYKELRLEVGKQRLKYAQEE 20
||||||||||||||||||||
Db 303 PYKELRLEVGKQRLKYAQEE 322

RESULT 2
POLG_HPAVG
ID POLG_HPAVG STANDARD; PRT; 808 AA.

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AC   Q02381;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEIN
DE   P2A] (FRAGMENT).
OS   Hepatitis A virus (strain GA76).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=31706;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92260183; PubMed=1316423;
RA   Khanna B., Spelbring J.E., Innis B.L., Robertson B.H.;
RT   "Characterization of a genetic variant of human hepatitis A virus.";
RL   J. Med. Virol. 36:118-124(1992).
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M66695; AAA45477.1; -.
KW   Polyprotein; Coat protein; Core protein.
FT   NON_TER       1      1
FT   CHAIN        <1      2       COAT PROTEIN VP4 (P1A).
FT   CHAIN         3    223       COAT PROTEIN VP2 (P1B).
FT   CHAIN       224    470       COAT PROTEIN VP3 (P1C).
FT   CHAIN       471    770       COAT PROTEIN VP1 (P1D).
FT   CHAIN       771   >808       CORE PROTEIN P2A.
FT   NON_TER     808    808
SQ   SEQUENCE   808 AA;  90632 MW;  D80CE7E57A479C12 CRC64;


  Query Match             100.0%;  Score 102;  DB 1;  Length 808;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db    778 PYKELRLEVGKQRLKYAQEE 797


RESULT   3
POLG_HPAVC
ID   POLG_HPAVC     STANDARD;      PRT;   852 AA.
AC   P06442; Q83741; Q83742;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEIN
DE   P2A] (FRAGMENT).
OS   Hepatitis A virus (strain CR326).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12097;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85185648; PubMed=2985793;
RA   Linemeyer D.L., Menke J.G., Martin-Gallardo A., Hughes J.V.,
RA   Young A., Mitra S.W.;
RT   "Molecular cloning and partial sequencing of hepatitis A viral cDNA.";
RL   J. Virol. 54:247-255(1985).
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M10033; AAA45470.1; -.
DR   PIR; A03904; GNNYHA.
KW   Polyprotein; Coat protein; Core protein.
FT   CHAIN         1     23       COAT PROTEIN VP4 (P1A).
FT   CHAIN        24    245       COAT PROTEIN VP2 (P1B).
FT   CHAIN       246    491       COAT PROTEIN VP3 (P1C).
FT   CHAIN       492    836       COAT PROTEIN VP1 (P1D).
FT   CHAIN       837   >852       CORE PROTEIN P2A.
FT   NON_TER     852    852
SQ   SEQUENCE   852 AA;  95563 MW;  73D3ED0AD532820E CRC64;


  Query Match             100.0%;  Score 102;  DB 1;  Length 852;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db    799 PYKELRLEVGKQRLKYAQEE 818


RESULT   4
POLG_HPAV2
ID   POLG_HPAV2     STANDARD;      PRT;  2226 AA.
AC   P26580;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
DE   P2A TO P2C; PROBABLE PROTEINS P3A TO P3C; RNA-DIRECTED RNA POLYMERASE
DE   P3D (EC 2.7.7.48)].
OS   Hepatitis A virus (strain 24a).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12094;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91162758; PubMed=1705995;
RA   Lemon S.M., Murphy P.C., Shields P.A., Ping L.H., Feinstone S.M.,
RA   Cromeans T., Jansen R.W.;
RT   "Antigenic and genetic variation in cytopathic hepatitis A virus
RT   variants arising during persistent infection: evidence for genetic
RT   recombination.";
RL   J. Virol. 65:2056-2065(1991).
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M59810; AAA45468.1; -.
DR   MEROPS; C03.005; -.
DR   InterPro; IPR000605; -.
DR   InterPro; IPR001205; -.
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DR   Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR   Pfam; PF00910; RNA_helicase; 1.
KW   Polyprotein; Coat protein; Core protein; Transferase;
KW   RNA-directed RNA polymerase; Hydrolase; Thiol protease.
FT   CHAIN         1     23       COAT PROTEIN VP4 (P1A).
FT   CHAIN        24    245       COAT PROTEIN VP2 (P1B).
FT   CHAIN       246    491       COAT PROTEIN VP3 (P1C).
FT   CHAIN       492    794       COAT PROTEIN VP1 (P1D).
FT   CHAIN       795    900       CORE PROTEIN P2A.
FT   CHAIN       901   1087       CORE PROTEIN P2B.
FT   CHAIN      1088   1422       CORE PROTEIN P2C.
FT   CHAIN      1423   1495       PROBABLE PROTEIN P3A.
FT   CHAIN      1496   1518       PROBABLE PROTEIN P3B.
FT   CHAIN      1519   1737       PROBABLE PROTEIN P3C.
FT   CHAIN      1738   2226       RNA-DIRECTED POLYMERASE P3D.
SQ   SEQUENCE   2226 AA;  251152 MW;  6CD85A91D6B4E2BF CRC64;


  Query Match             100.0%;  Score 102;  DB 1;  Length 2226;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db    799 PYKELRLEVGKQRLKYAQEE 818


RESULT   5
POLG_HPAV4
ID   POLG_HPAV4     STANDARD;      PRT;  2226 AA.
AC   P26581;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
DE   P2A TO P2C; PROBABLE PROTEINS P3A TO P3C; RNA-DIRECTED RNA POLYMERASE
DE   P3D (EC 2.7.7.48)].
OS   Hepatitis A virus (strain 43c).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12095;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91162758; PubMed=1705995;
RA   Lemon S.M., Murphy P.C., Shields P.A., Ping L.H., Feinstone S.M.,
RA   Cromeans T., Jansen R.W.;
RT   "Antigenic and genetic variation in cytopathic hepatitis A virus
RT   variants arising during persistent infection: evidence for genetic
RT   recombination.";
RL   J. Virol. 65:2056-2065(1991).
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M59809; AAA45469.1; -.
DR   MEROPS; C03.005; -.
DR   InterPro; IPR000605; -.
DR   InterPro; IPR001205; -.
DR   Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR   Pfam; PF00910; RNA_helicase; 1.
KW   Polyprotein; Coat protein; Core protein; Transferase;
KW   RNA-directed RNA polymerase; Hydrolase; Thiol protease.
FT   CHAIN         1     23       COAT PROTEIN VP4 (P1A).
FT   CHAIN        24    245       COAT PROTEIN VP2 (P1B).
FT   CHAIN       246    491       COAT PROTEIN VP3 (P1C).
FT   CHAIN       492    794       COAT PROTEIN VP1 (P1D).
FT   CHAIN       795    900       CORE PROTEIN P2A.
FT   CHAIN       901   1087       CORE PROTEIN P2B.
FT   CHAIN      1088   1422       CORE PROTEIN P2C.
FT   CHAIN      1423   1495       PROBABLE PROTEIN P3A.
FT   CHAIN      1496   1518       PROBABLE PROTEIN P3B.
FT   CHAIN      1519   1737       PROBABLE PROTEIN P3C.
FT   CHAIN      1738   2226       RNA-DIRECTED POLYMERASE P3D.
SQ   SEQUENCE   2226 AA;  251107 MW;  403B4CA80B09BF75 CRC64;


  Query Match             100.0%;  Score 102;  DB 1;  Length 2226;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db    799 PYKELRLEVGKQRLKYAQEE 818


RESULT   6
POLG_HPAV8
ID   POLG_HPAV8     STANDARD;      PRT;  2226 AA.
AC   P26582;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
DE   P2A TO P2C; PROBABLE PROTEINS P3A TO P3C; RNA-DIRECTED RNA POLYMERASE
DE   P3D (EC 2.7.7.48)].
OS   Hepatitis A virus (strain 18f).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12096;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91162758; PubMed=1705995;
RA   Lemon S.M., Murphy P.C., Shields P.A., Ping L.H., Feinstone S.M.,
RA   Cromeans T., Jansen R.W.;
RT   "Antigenic and genetic variation in cytopathic hepatitis A virus
RT   variants arising during persistent infection: evidence for genetic
RT   recombination.";
RL   J. Virol. 65:2056-2065(1991).
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
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CC   ---------------------------------------------------------------------
DR   EMBL; M59808; AAA45467.1; -.
DR   MEROPS; C03.005; -.
DR   InterPro; IPR000605; -.
DR   InterPro; IPR001205; -.
DR   Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR   Pfam; PF00910; RNA_helicase; 1.
KW   Polyprotein; Coat protein; Core protein; Transferase;
KW   RNA-directed RNA polymerase; Hydrolase; Thiol protease.
FT   CHAIN         1     23       COAT PROTEIN VP4 (P1A).
FT   CHAIN        24    245       COAT PROTEIN VP2 (P1B).
FT   CHAIN       246    491       COAT PROTEIN VP3 (P1C).
FT   CHAIN       492    794       COAT PROTEIN VP1 (P1D).
FT   CHAIN       795    900       CORE PROTEIN P2A.
FT   CHAIN       901   1087       CORE PROTEIN P2B.
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FT   CHAIN      1088   1422       CORE PROTEIN P2C.
FT   CHAIN      1423   1495       PROBABLE PROTEIN P3A.
FT   CHAIN      1496   1518       PROBABLE PROTEIN P3B.
FT   CHAIN      1519   1737       PROBABLE PROTEIN P3C.
FT   CHAIN      1738   2226       RNA-DIRECTED POLYMERASE P3D.
SQ   SEQUENCE   2226 AA;  251292 MW;  24964A63396C8D6B CRC64;


  Query Match             100.0%;  Score 102;  DB 1;  Length 2226;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db    799 PYKELRLEVGKQRLKYAQEE 818


RESULT   7
POLG_HPAVH
ID   POLG_HPAVH     STANDARD;      PRT;  2227 AA.
AC   P08617; P06443; Q81082;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
DE   P2A TO P2C; PROBABLE PROTEINS P3A TO P3C; RNA-DIRECTED RNA POLYMERASE
DE   P3D (EC 2.7.7.48)].
OS   Hepatitis A virus (strain HM-175).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12098;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WILD TYPE;
RX   MEDLINE=87061253; PubMed=3023706;
RA   Cohen J.I., Ticehurst J.R., Purcell R.H., Buckler-White A.,
RA   Baroudy B.M.;
RT   "Complete nucleotide sequence of wild-type hepatitis A virus:
RT   comparison with different strains of hepatitis A virus and other
RT   picornaviruses.";
RL   J. Virol. 61:50-59(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATTENUATED;
RX   MEDLINE=87175701; PubMed=3031686;
RA   Cohen J.I., Rosenblum B., Ticehurst J.R., Daemer R.J., Feinstone S.M.,
RA   Purcell R.H.;
RT   "Complete nucleotide sequence of an attenuated hepatitis A virus:
RT   comparison with wild-type virus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:2497-2501(1987).
RN   [3]
RP   SEQUENCE OF 1-854 AND 1724-2227 FROM N.A.
RX   MEDLINE=85166289; PubMed=2984684;
RA   Baroudy B.M., Ticehurst J.R., Miele T.A., Maizel J.V. Jr.,
RA   Purcell R.H., Feinstone S.M.;
RT   "Sequence analysis of hepatitis A virus cDNA coding for capsid
RT   proteins and RNA polymerase.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:2143-2147(1985).
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- MISCELLANEOUS: STRAIN HM-175/7 MK-5 IS ATTENUATED STRAIN DERIVED
CC       FROM HM-175 BY 32 PASSAGES IN AFRICAN GREEN MONKEY KIDNEY CELLS.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC   -!- CAUTION: REF.3 SEQUENCE HAS A NUMBER OF CONFLICTS WITH THAT
CC       SHOWN.
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M14114; AAA45475.1; -.
DR   EMBL; M14707; AAA45465.1; -.
DR   EMBL; M14707; AAA45466.1; ALT_INIT.
DR   EMBL; M16632; AAA45471.1; -.
DR   PIR; A25981; GNNYHM.
DR   PIR; A25914; GNNYMK.
DR   PIR; A03905; A03905.
DR   MEROPS; C03.005; -.
DR   InterPro; IPR000605; -.
DR   InterPro; IPR001205; -.
DR   Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR   Pfam; PF00910; RNA_helicase; 1.
KW   Polyprotein; Coat protein; Core protein; Transferase;
KW   RNA-directed RNA polymerase; Hydrolase; Thiol protease.
FT   CHAIN         1     23       COAT PROTEIN VP4 (P1A).
FT   CHAIN        24    245       COAT PROTEIN VP2 (P1B).
FT   CHAIN       246    491       COAT PROTEIN VP3 (P1C).
FT   CHAIN       492    836       COAT PROTEIN VP1 (P1D).
FT   CHAIN       837    980       CORE PROTEIN P2A.
FT   CHAIN       981   1087       CORE PROTEIN P2B.
FT   CHAIN      1088   1422       CORE PROTEIN P2C.
FT   CHAIN      1423   1496       PROBABLE PROTEIN P3A.
FT   CHAIN      1497   1519       PROBABLE PROTEIN P3B.
FT   CHAIN      1520   1738       PROBABLE PROTEIN P3C.
FT   CHAIN      1739   2227       RNA-DIRECTED POLYMERASE 3D.
FT   VARIANT      77     77       K -> R (IN ATTENUATED STRAIN).
FT   VARIANT     764    764       E -> V (IN ATTENUATED STRAIN).
FT   VARIANT     821    821       N -> S (IN ATTENUATED STRAIN).
FT   VARIANT    1052   1052       A -> V (IN ATTENUATED STRAIN).
FT   VARIANT    1062   1062       G -> A (IN ATTENUATED STRAIN).
FT   VARIANT    1118   1118       K -> M (IN ATTENUATED STRAIN).
FT   VARIANT    1151   1151       E -> K (IN ATTENUATED STRAIN).
FT   VARIANT    1163   1163       F -> S (IN ATTENUATED STRAIN).
FT   VARIANT    1277   1277       V -> I (IN ATTENUATED STRAIN).
FT   VARIANT    1500   1500       H -> Y (IN ATTENUATED STRAIN).
FT   VARIANT    1805   1805       D -> N (IN ATTENUATED STRAIN).
FT   VARIANT    1930   1930       S -> T (IN ATTENUATED STRAIN).
SQ   SEQUENCE   2227 AA;  251506 MW;  01E225E7AEB740A6 CRC64;


  Query Match             100.0%;  Score 102;  DB 1;  Length 2227;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db    799 PYKELRLEVGKQRLKYAQEE 818


RESULT   8
POLG_HPAVL
ID   POLG_HPAVL     STANDARD;      PRT;  2227 AA.
AC   P06441;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
DE   P2A TO P2C; PROBABLE PROTEINS P3A TO P3C; RNA-DIRECTED RNA POLYMERASE
DE   P3D (EC 2.7.7.48)].
OS   Hepatitis A virus (strain LA).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12099;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85190549; PubMed=2986127;
RA   Najarian R., Caput D., Gee W.W., Potter S.J., Renard A.,
RA   Merryweather J., van Nest G., Dina D.;
RT   "Primary structure and gene organization of human hepatitis A virus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:2627-2631(1985).
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CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K02990; AAA45472.1; -.
DR   PIR; A03903; GNNYHR.
DR   MEROPS; C03.005; -.
DR   InterPro; IPR000605; -.
DR   InterPro; IPR001205; -.
DR   Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR   Pfam; PF00910; RNA_helicase; 1.
KW   Polyprotein; Coat protein; Core protein; Transferase;
KW   RNA-directed RNA polymerase; Hydrolase; Thiol protease.
FT   CHAIN         1     23       COAT PROTEIN VP4 (P1A).
FT   CHAIN        24    245       COAT PROTEIN VP2 (P1B).
FT   CHAIN       246    491       COAT PROTEIN VP3 (P1C).
FT   CHAIN       492    836       COAT PROTEIN VP1 (P1D).
FT   CHAIN       837    980       CORE PROTEIN P2A.
FT   CHAIN       981   1076       CORE PROTEIN P2B.
FT   CHAIN      1077   1422       CORE PROTEIN P2C.
FT   CHAIN      1423   1484       PROBABLE PROTEIN P3A.
FT   CHAIN      1485   1507       PROBABLE PROTEIN P3B.
FT   CHAIN      1508   1678       PROBABLE PROTEIN P3C.
FT   CHAIN      1679   2227       RNA-DIRECTED POLYMERASE P3D.
SQ   SEQUENCE   2227 AA;  251898 MW;  99A7354B4CD2799C CRC64;


  Query Match             100.0%;  Score 102;  DB 1;  Length 2227;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 PYKELRLEVGKQRLKYAQEE 20
           ||||||||||||||||||||
Db     799 PYKELRLEVGKQRLKYAQEE 818


RESULT   9
POLG_HPAVM
ID   POLG_HPAVM     STANDARD;      PRT;  2227 AA.
AC   P13901; Q81083; Q81084; Q81085; Q81086; Q81087; Q81088; Q81089;
AC   Q81090; Q81091; Q81092; Q81093;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
DE   P2A TO P2C; PROBABLE PROTEINS P3A TO P3C; RNA-DIRECTED RNA POLYMERASE
DE   P3D (EC 2.7.7.48)].
OS   Hepatitis A virus (strain MBB).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12100;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88045071; PubMed=2823500;
RA   Paul A.V., Tada H., der Helm K., Wissel T., Kiehn R., Wimmer E.,
RA   Deinhardt F.;
RT   "The entire nucleotide sequence of the genome of human hepatitis A
RT   virus (isolate MBB).";
RL   Virus Res. 8:153-171(1987).
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- MISCELLANEOUS: THIS VIRUS WAS ISOLATED FROM THE STOOL OF A PATIENT
CC       WHO HAD BEEN INFECTED IN THE AFRICAN MEDITERRANEAN REGION.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M20273; AAA45474.1; -.
DR   PIR; JS0303; GNNYHB.
DR   MEROPS; C03.005; -.
DR   InterPro; IPR000605; -.
DR   InterPro; IPR001205; -.
DR   Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR   Pfam; PF00910; RNA_helicase; 1.
KW   Polyprotein; Coat protein; Core protein; Transferase;
KW   RNA-directed RNA polymerase; Hydrolase; Thiol protease.
FT   CHAIN         1     23       COAT PROTEIN VP4 (P1A).
FT   CHAIN        24    245       COAT PROTEIN VP2 (P1B).
FT   CHAIN       246    491       COAT PROTEIN VP3 (P1C).
FT   CHAIN       492    836       COAT PROTEIN VP1 (P1D).
FT   CHAIN       837    980       CORE PROTEIN P2A.
FT   CHAIN       981   1087       CORE PROTEIN P2B.
FT   CHAIN      1088   1422       CORE PROTEIN P2C.
FT   CHAIN      1423   1496       PROBABLE PROTEIN P3A.
FT   CHAIN      1497   1519       PROBABLE PROTEIN P3B.
FT   CHAIN      1520   1738       PROBABLE PROTEIN P3C.
FT   CHAIN      1739   2227       RNA-DIRECTED POLYMERASE 3D.
SQ   SEQUENCE   2227 AA;  251425 MW;  EC983ED2A7C86349 CRC64;


  Query Match             100.0%;  Score 102;  DB 1;  Length 2227;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 PYKELRLEVGKQRLKYAQEE 20
           ||||||||||||||||||||
Db     799 PYKELRLEVGKQRLKYAQEE 818


RESULT  10
POLG_HPAVS
ID   POLG_HPAVS     STANDARD;      PRT;  2230 AA.
AC   P14553;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
DE   P2A TO P2C; PROBABLE PROTEINS P3A TO P3C; RNA-DIRECTED RNA POLYMERASE
DE   P3D (EC 2.7.7.48)].
OS   Simian hepatitis A virus (strain AGM-27).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12102;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91311420; PubMed=1649901;
RA   Tsarev S.A., Emerson S.U., Balayan M.S., Ticehurst J.R.,
RA   Purcell R.H.;
RT   "Simian hepatitis A virus (HAV) strain AGM-27: comparison of genome
RT   structure and growth in cell culture with other HAV strains.";
RL   J. Gen. Virol. 72:1677-1683(1991).
RN   [2]
RP   SEQUENCE OF 1750-2164 FROM N.A.
RX   MEDLINE=89232168; PubMed=2541023;
RA   Balayan M.S., Kusov Y.Y., Andjaparidze A.G., Tsarev S.A.,
RA   Sverdlov E.D., Chizhikov V.E., Blinov V.M., Vasilenko S.K.;
RT   "Variations in genome fragments coding for RNA polymerase in human
RT   and simian hepatitis A viruses.";
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RL   FEBS Lett. 247:425-428(1989).
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; D00924; BAA00766.1; -.
DR   EMBL; X15461; CAA33490.1; -.
DR   PIR; A30470; GNNYSA.
DR   PIR; S04885; S04885.
DR   MEROPS; C03.005; -.
DR   InterPro; IPR000605; -.
DR   InterPro; IPR001205; -.
DR   Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR   Pfam; PF00910; RNA_helicase; 1.
KW   Polyprotein; Coat protein; Core protein; Transferase;
KW   RNA-directed RNA polymerase; Hydrolase; Thiol protease.
FT   CHAIN         1     27       COAT PROTEIN VP4 (P1A).
FT   CHAIN        28    249       COAT PROTEIN VP2 (P1B).
FT   CHAIN       250    495       COAT PROTEIN VP3 (P1C).
FT   CHAIN       496    795       COAT PROTEIN VP1 (P1D).
FT   CHAIN       796    984       CORE PROTEIN P2A.
FT   CHAIN       985   1091       CORE PROTEIN P2B.
FT   CHAIN      1092   1426       CORE PROTEIN P2C.
FT   CHAIN      1427   1498       PROBABLE PROTEIN 3A.
FT   CHAIN      1499   1521       PROBABLE PROTEIN 3B.
FT   CHAIN      1522   1741       PROBABLE PROTEIN 3C.
FT   CHAIN      1742   2230       RNA-DIRECTED POLYMERASE 3D.
SQ   SEQUENCE   2230 AA;  251296 MW;  87B3230E324E1F19 CRC64;


  Query Match             93.1%;  Score 95;  DB 1;  Length 2230;
  Best Local Similarity   90.0%;  Pred. No. 6.2e-07;
  Matches   18;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 PYKELRLEVGKQRLKYAQEE 20
           |||||:||||||||||| ||
Db     803 PYKELRMEVGKQRLKYAMEE 822


RESULT  11
POLG_HPAVT
ID   POLG_HPAVT     STANDARD;      PRT;   839 AA.
AC   P31788;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEIN
DE   P2A] (FRAGMENT).
OS   Simian hepatitis A virus (strain CY-145).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=31707;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91311421; PubMed=1649902;
RA   Nainan O.V., Margolis H.S., Robertson B.H., Balayan M., Brinton M.A.;
RT   "Sequence analysis of a new hepatitis A virus naturally infecting
RT   cynomolgus macaques (Macaca fascicularis).";
RL   J. Gen. Virol. 72:1685-1689(1991).
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M59286; AAA45473.1; -.
DR   PIR; JQ1180; GNNYS2.
KW   Polyprotein; Coat protein; Core protein.
FT   CHAIN         1     23       COAT PROTEIN VP4 (P1A).
FT   CHAIN        24    245       COAT PROTEIN VP2 (P1B).
FT   CHAIN       246    491       COAT PROTEIN VP3 (P1C).
FT   CHAIN       492      ?       COAT PROTEIN VP1 (P1D).
FT   CHAIN         ?   >839       CORE PROTEIN P2A.
FT   NON_TER     839    839
SQ   SEQUENCE   839 AA;  93825 MW;  2CACC4BD1E192DBC CRC64;


  Query Match             92.2%;  Score 94;  DB 1;  Length 839;
  Best Local Similarity   90.0%;  Pred. No. 3.1e-07;
  Matches   18;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 PYKELRLEVGKQRLKYAQEE 20
           |||||||||||||| |||:||
Db     798 PYKELRLEVGKQRFKYAREE 817


RESULT  12
VATD_CHLPN
ID   VATD_CHLPN     STANDARD;      PRT;   209 AA.
AC   Q9Z991;
DT   01-OCT-2000 (Rel. 40, Created)
DT   01-OCT-2000 (Rel. 40, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   V-TYPE ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-TYPE ATPASE SUBUNIT D).
GN   ATPD OR CPN0090 OR CP0684.
OS   Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC   Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX   NCBI_TaxID=83558;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CWL029;
RX   MEDLINE=99206606; PubMed=10192388;
RA   Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA   Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT   "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL   Nat. Genet. 21:385-389(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AR39;
RX   MEDLINE=20150255; PubMed=10684935;
RA   Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA   White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T.,
RA   Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B.,
RA   Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J.,
RA   McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
RT   "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT   pneumoniae AR39.";
RL   Nucleic Acids Res. 28:1397-1406(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=J138;
RX   MEDLINE=20330349; PubMed=10871362;
RA   Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA   Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT   "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT   from Japan and CWL029 from USA.";
RL   Nucleic Acids Res. 28:2311-2314(2000).
CC   -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC       GRADIENT ACROSS THE MEMBRANE.
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CC   -!- SIMILARITY: BELONGS TO THE V-ATPASE D SUBUNIT FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AE001594; AAD18243.1; -.
DR   EMBL; AE002227; AAF73696.1; -.
DR   EMBL; AP002545; BAA98300.1; -.
DR   TIGR; CP0684; -.
DR   InterPro; IPR002699; -.
DR   Pfam; PF01813; ATP-synt_D; 1.
KW   Hydrolase; ATP synthesis; Hydrogen ion transport.
SQ   SEQUENCE   209 AA;  23788 MW;  D40A5C36313FEEBF CRC64;


  Query Match             44.1%;  Score 45;  DB 1;  Length 209;
  Best Local Similarity   50.0%;  Pred. No. 4;
  Matches    9;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       3 KELRLEVGKQRLKYAQEE 20
           |::  || |:|||  :||
Db     133 KKVMAEVSKERLKILEEE 150


RESULT  13
ILVE_RICPR
ID   ILVE_RICPR     STANDARD;      PRT;   290 AA.
AC   O05970;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   PROBABLE BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
DE   (BCAT).
GN   ILVE OR RP428.
OS   Rickettsia prowazekii.
OC   Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC   Rickettsiaceae; Rickettsieae; Rickettsia.
OX   NCBI_TaxID=782;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MADRID E;
RX   MEDLINE=97419517; PubMed=9274032;
RA   Andersson J.O., Andersson S.G.E.;
RT   "Genomic rearrangements during evolution of the obligate
RT   intracellular parasite Rickettsia prowazekii as inferred from an
RT   analysis of 52015 bp nucleotide sequence.";
RL   Microbiology 143:2783-2795(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MADRID E;
RX   MEDLINE=99039499; PubMed=9823893;
RA   Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA   Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA   Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT   "The genome sequence of Rickettsia prowazekii and the origin of
RT   mitochondria.";
RL   Nature 396:133-140(1998).
CC   -!- CATALYTIC ACTIVITY: L-LEUCINE + 2-OXOGLUTARATE = 4-METHYL-2-
CC       OXOPENTANOATE + L-GLUTAMATE (ALSO ACTS ON L-ISOLEUCINE AND
CC       L-VALINE).
CC   -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC   -!- PATHWAY: VALINE AND ISOLEUCINE BIOSYNTHESIS.
CC   -!- SIMILARITY: BELONGS TO CLASS-IV OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC       AMINOTRANSFERASES.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y11777; CAA72450.1; -.
DR   EMBL; AJ235271; CAA14885.1; -.
DR   InterPro; IPR001544; -.
DR   Pfam; PF01063; aminotran_4; 1.
DR   PROSITE; PS00770; AA_TRANSFER_CLASS_4; 1.
KW   Transferase; Aminotransferase; Branched-chain amino acid biosynthesis;
KW   Pyridoxal phosphate.
FT   BINDING     155    155       PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ   SEQUENCE   290 AA;  33068 MW;  98374E325350763D CRC64;


  Query Match             43.1%;  Score 44;  DB 1;  Length 290;
  Best Local Similarity   61.1%;  Pred. No. 8.2;
  Matches   11;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       3 KELRLEVGKQRLKYAQEE 20
           | | ||| ::||| || |
Db     225 KSLCLEVKEERLKLAQIE 242


RESULT  14
FOJO_DROME
ID   FOJO_DROME     STANDARD;      PRT;   583 AA.
AC   P54360; Q24176;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   FOUR-JOINTED PROTEIN.
GN   FJ.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye imaginal disk;
RX   MEDLINE=96038089; PubMed=7555705;
RA   Villano J.L., Katz F.N.;
RT   "four-jointed is required for intermediate growth in the proximal-
RT   distal axis in Drosophila.";
RL   Development 121:2767-2777(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CANTON-S;
RX   MEDLINE=96187865; PubMed=8606003;
RA   Brodsky M.H., Steller H.;
RT   "Positional information along the dorsal-ventral axis of the
RT   Drosophila eye: graded expression of the four-jointed gene.";
RL   Dev. Biol. 173:428-446(1996).
CC   -!- FUNCTION: REQUIRED FOR INTERMEDIATE GROWTH IN THE PROXIMAL-DISTAL
CC       AXIS. MAY BE REQUIRED FOR CELL-CELL SIGNALING DURING DISC
CC       DEVELOPMENT.
CC   -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U28837; AAA69524.1; -.
DR   EMBL; U44904; AAB01809.1; -.
DR   FlyBase; FBgn0000658; fj.
KW   Transmembrane; Signal-anchor.
FT   DOMAIN        1     78       CYTOPLASMIC (POTENTIAL).
```

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FT   TRANSMEM     79     99       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN      100    583       EXTRACELLULAR (POTENTIAL).
FT   CARBOHYD    310    310       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    379    379       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    491    491       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    126    126       T -> S (IN REF. 2).
FT   CONFLICT    193    193       M -> L (IN REF. 2).
FT   CONFLICT    288    288       P -> R (IN REF. 2).
FT   CONFLICT    330    330       R -> A (IN REF. 2).
SQ   SEQUENCE   583 AA;  65504 MW;  82F1EA2A299DB284 CRC64;


  Query Match             43.1%;  Score 44;  DB 1;  Length 583;
  Best Local Similarity   50.0%;  Pred. No. 17;
  Matches    9;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2 YKELRLEVGKQRLKYAQE 19
           |   ||| |:|:|: ||:
Db       2 YDIKRLEAGQQKLQQAQQ 19


RESULT  15
UPP_AQUAE
ID   UPP_AQUAE      STANDARD;      PRT;   208 AA.
AC   O67914;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9) (UMP PYROPHOSPHORYLASE)
DE   (UPRTASE).
GN   UPP OR URAP OR AQ_2163.
OS   Aquifex aeolicus.
OC   Bacteria; Aquificales; Aquificaceae; Aquifex.
OX   NCBI_TaxID=63363;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VF5;
RX   MEDLINE=98196666; PubMed=9537320;
RA   Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA   Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA   Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT   "The complete genome of the hyperthermophilic bacterium Aquifex
RT   aeolicus.";
RL   Nature 392:353-358(1998).
CC   -!- CATALYTIC ACTIVITY: UMP + PYROPHOSPHATE = URACIL + 5-PHOSPHO-
CC       ALPHA-D-RIBOSE 1-DIPHOSPHATE.
CC   -!- PATHWAY: PYRIMIDINE SALVAGE PATHWAY.
CC   -!- SIMILARITY: BELONGS TO THE UPRTASE FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AE000776; AAC07880.1; -.
DR   InterPro; IPR000836; -.
DR   Pfam; PF00156; Pribosyltran; 1.
KW   Transferase; Glycosyltransferase.
SQ   SEQUENCE   208 AA;  23532 MW;  87B9CFEFEA9CFF77 CRC64;


  Query Match             42.2%;  Score 43;  DB 1;  Length 208;
  Best Local Similarity   44.4%;  Pred. No. 8.3;
  Matches    8;  Conservative    3;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       3 KELRLEVGKQRLKYAQEE 20
           ||:|  :| :|  |  ||
Db      51 KEVRTWIGNKRFNYLNEE 68
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Search completed: April 24, 2001, 16:33:55
Job time: 551 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2001, 16:33:07 ; Search time 113.97 Seconds
(without alignments)
20.568 Million cell updates/sec

Title: US-09-171-432A-40
Perfect score: 102
Sequence: 1 PYKELRLEVGKQRLKYAQEE 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	102	100.0	56	14	Q67818	Q67818 hepatitis a
2	102	100.0	56	14	Q67819	Q67819 hepatitis a
3	102	100.0	56	14	Q67820	Q67820 hepatitis a
4	102	100.0	56	14	Q67821	Q67821 hepatitis a
5	102	100.0	56	14	Q67822	Q67822 hepatitis a
6	102	100.0	56	14	Q67823	Q67823 hepatitis a
7	102	100.0	56	14	O39865	O39865 hepatitis a
8	102	100.0	56	14	O39866	O39866 hepatitis a
9	102	100.0	56	14	O39867	O39867 hepatitis a
10	102	100.0	56	14	O39868	O39868 hepatitis a
11	102	100.0	56	14	O39869	O39869 hepatitis a
12	102	100.0	56	14	O39870	O39870 hepatitis a
13	102	100.0	56	14	O39871	O39871 hepatitis a
14	102	100.0	56	14	O39872	O39872 hepatitis a
15	102	100.0	56	14	O39873	O39873 hepatitis a
16	102	100.0	56	14	O39874	O39874 hepatitis a
17	102	100.0	56	14	Q96829	Q96829 hepatitis a
18	102	100.0	56	14	Q96830	Q96830 hepatitis a
19	102	100.0	56	14	Q9IPD2	Q9ipd2 hepatitis a
20	102	100.0	56	14	Q9IPD1	Q9ipd1 hepatitis a
21	102	100.0	56	14	Q9IPC9	Q9ipc9 hepatitis a
22	102	100.0	56	14	Q9IPC8	Q9ipc8 hepatitis a
23	102	100.0	56	14	Q9IPC7	Q9ipc7 hepatitis a
24	102	100.0	56	14	Q9IPC5	Q9ipc5 hepatitis a
25	102	100.0	56	14	Q9IPC4	Q9ipc4 hepatitis a
26	102	100.0	56	14	Q9IPC3	Q9ipc3 hepatitis a
27	102	100.0	56	14	Q9IPC2	Q9ipc2 hepatitis a
28	102	100.0	56	14	Q9IPC1	Q9ipc1 hepatitis a
29	102	100.0	56	14	Q9IPC0	Q9ipc0 hepatitis a
30	102	100.0	56	14	Q9IPB9	Q9ipb9 hepatitis a
31	102	100.0	56	14	Q9IPB8	Q9ipb8 hepatitis a
32	102	100.0	56	14	Q9IPB6	Q9ipb6 hepatitis a
33	102	100.0	56	14	Q9IPB5	Q9ipb5 hepatitis a
34	102	100.0	56	14	Q9IPB4	Q9ipb4 hepatitis a
35	102	100.0	56	14	Q9IPB3	Q9ipb3 hepatitis a
36	102	100.0	56	14	Q9IPB2	Q9ipb2 hepatitis a
37	102	100.0	56	14	Q9IPB1	Q9ipb1 hepatitis a
38	102	100.0	56	14	Q9IPB0	Q9ipb0 hepatitis a
39	102	100.0	56	14	Q9IPA9	Q9ipa9 hepatitis a
40	102	100.0	56	14	Q9IPA8	Q9ipa8 hepatitis a
41	102	100.0	56	14	Q9IPA7	Q9ipa7 hepatitis a
42	102	100.0	56	14	Q9IPA6	Q9ipa6 hepatitis a
43	102	100.0	56	14	Q9IPA5	Q9ipa5 hepatitis a
44	102	100.0	56	14	Q9IPA4	Q9ipa4 hepatitis a
45	102	100.0	56	14	Q9IP87	Q9ip87 hepatitis a

ALIGNMENTS

RESULT 1
Q67818
ID Q67818 PRELIMINARY; PRT; 56 AA.
AC Q67818;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE POLYPROTEIN (FRAGMENTS).
OS Hepatitis A virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Hepatovirus.
OX NCBI_TaxID=12092;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ISR-05, AFULA DISTRICT, ISRAEL, 1993;
RA Karetnyi Y.V., Shulman L.M., Manor J., Leitner L., Shehab S.,
RA Mendelson E.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Z77243; CAB01036.1; -.
DR INTERPRO; IPR000886; -.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Polyprotein; Nonstructural protein.
FT NON_TER 1 1
FT CHAIN 1 >28 CAPSID PROTEIN VP1.
FT NON_CONS 28 29
FT CHAIN 29 >56 NONSTRUCTURAL PROTEIN NS2A.
FT NON_TER 56 56
SQ SEQUENCE 56 AA; 6614 MW; 8438C51846AEF4A4 CRC64;

Query Match 100.0%; Score 102; DB 14; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYKELRLEVGKQRLKYAQEE 20
||||||||||||||||||||
Db 36 PYKELRLEVGKQRLKYAQEE 55

RESULT 2
Q67819
ID Q67819 PRELIMINARY; PRT; 56 AA.

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AC   Q67819;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENTS).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ISR-10, (AFULA DISTRICT, ISRAEL, 1993);
RA   Karetnyi Y.V., Shulman L.M., Manor J., Leitner L., Shehab S.,
RA   Mendelson E.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77244; CAB01037.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein; Nonstructural protein.
FT   NON_TER       1      1
FT   CHAIN         1    >28       CAPSID PROTEIN VP1.
FT   NON_CONS     28     29
FT   CHAIN        29    >56       NONSTRUCTURAL PROTEIN NS2A.
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;

  Query Match            100.0%;  Score 102;  DB 14;  Length 56;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db     36 PYKELRLEVGKQRLKYAQEE 55


RESULT   3
Q67820
ID   Q67820      PRELIMINARY;      PRT;    56 AA.
AC   Q67820;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENTS).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ISR-12, (AFULA DISTRICT, ISRAEL, 1993);
RA   Karetnyi Y.V., Shulman L.M., Manor J., Leitner L., Shehab S.,
RA   Mendelson E.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77245; CAB01038.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein; Nonstructural protein.
FT   NON_TER       1      1
FT   CHAIN         1    >28       CAPSID PROTEIN VP1.
FT   NON_CONS     28     29
FT   CHAIN        29    >56       NONSTRUCTURAL PROTEIN NS2A.
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;

  Query Match            100.0%;  Score 102;  DB 14;  Length 56;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db     36 PYKELRLEVGKQRLKYAQEE 55


RESULT   4
Q67821
ID   Q67821      PRELIMINARY;      PRT;    56 AA.
AC   Q67821;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENTS).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ISR-15, (AFULA DISTRICT, ISRAEL, 1993);
RA   Karetnyi Y.V., Shulman L.M., Manor J., Leitner L., Shehab S.,
RA   Mendelson E.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77246; CAB01039.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein; Nonstructural protein.
FT   NON_TER       1      1
FT   CHAIN         1    >28       CAPSID PROTEIN VP1.
FT   NON_CONS     28     29
FT   CHAIN        29    >56       NONSTRUCTURAL PROTEIN NS2A.
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;

  Query Match            100.0%;  Score 102;  DB 14;  Length 56;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db     36 PYKELRLEVGKQRLKYAQEE 55


RESULT   5
Q67822
ID   Q67822      PRELIMINARY;      PRT;    56 AA.
AC   Q67822;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENTS).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ISR-70, (AKKO DISTRICT, ISRAEL, 1993);
RA   Karetnyi Y.V., Shulman L.M., Manor J., Leitner L., Shehab S.,
RA   Mendelson E.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77247; CAB01040.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein; Nonstructural protein.
FT   NON_TER       1      1
FT   CHAIN         1    >28       CAPSID PROTEIN VP1.
FT   NON_CONS     28     29
FT   CHAIN        29    >56       NONSTRUCTURAL PROTEIN NS2A.
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;

  Query Match            100.0%;  Score 102;  DB 14;  Length 56;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-08;
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db     36 PYKELRLEVGKQRLKYAQEE 55


RESULT   6
Q67823
ID   Q67823      PRELIMINARY;      PRT;    56 AA.
AC   Q67823;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENTS).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ISR-79, (AKKO DISTRICT, ISRAEL, 1993);
RA   Karetnyi Y.V., Shulman L.M., Manor J., Leitner L., Shehab S.,
RA   Mendelson E.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77248; CAB01041.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein; Nonstructural protein.
FT   NON_TER       1      1
FT   CHAIN         1    >28       CAPSID PROTEIN VP1.
FT   NON_CONS     28     29
FT   CHAIN        29    >56       NONSTRUCTURAL PROTEIN NS2A.
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;

  Query Match             100.0%;  Score 102;  DB 14;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db     36 PYKELRLEVGKQRLKYAQEE 55


RESULT   7
O39865
ID   O39865      PRELIMINARY;      PRT;    56 AA.
AC   O39865;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENT).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=412991;
RX   MEDLINE=97247817; PubMed=9093940;
RA   Taylor M.B.;
RT   "Molecular epidemiology of South African strains of hepatitis A virus:
RT   1982-1996.";
RL   J. Med. Virol. 51:273-279(1997).
DR   EMBL; U68689; AAB53585.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein.
FT   NON_TER       1      1
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;

  Query Match             100.0%;  Score 102;  DB 14;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db     36 PYKELRLEVGKQRLKYAQEE 55


RESULT   8
O39866
ID   O39866      PRELIMINARY;      PRT;    56 AA.
AC   O39866;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENT).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=96001190;
RX   MEDLINE=97247817; PubMed=9093940;
RA   Taylor M.B.;
RT   "Molecular epidemiology of South African strains of hepatitis A virus:
RT   1982-1996.";
RL   J. Med. Virol. 51:273-279(1997).
DR   EMBL; U68690; AAB53586.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein.
FT   NON_TER       1      1
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;

  Query Match             100.0%;  Score 102;  DB 14;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db     36 PYKELRLEVGKQRLKYAQEE 55


RESULT   9
O39867
ID   O39867      PRELIMINARY;      PRT;    56 AA.
AC   O39867;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENT).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JVR;
RX   MEDLINE=97247817; PubMed=9093940;
RA   Taylor M.B.;
RT   "Molecular epidemiology of South African strains of hepatitis A virus:
RT   1982-1996.";
RL   J. Med. Virol. 51:273-279(1997).
DR   EMBL; U68692; AAB53588.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein.
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FT   NON_TER       1      1
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;


  Query Match             100.0%;  Score 102;  DB 14;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db     36 PYKELRLEVGKQRLKYAQEE 55


RESULT  10
O39868
ID   O39868      PRELIMINARY;      PRT;    56 AA.
AC   O39868;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENT).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=503712;
RX   MEDLINE=97247817; PubMed=9093940;
RA   Taylor M.B.;
RT   "Molecular epidemiology of South African strains of hepatitis A virus:
RT   1982-1996.";
RL   J. Med. Virol. 51:273-279(1997).
DR   EMBL; U68693; AAB53589.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein.
FT   NON_TER       1      1
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;


  Query Match             100.0%;  Score 102;  DB 14;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db     36 PYKELRLEVGKQRLKYAQEE 55


RESULT  11
O39869
ID   O39869      PRELIMINARY;      PRT;    56 AA.
AC   O39869;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENT).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=96002382;
RX   MEDLINE=97247817; PubMed=9093940;
RA   Taylor M.B.;
RT   "Molecular epidemiology of South African strains of hepatitis A virus:
RT   1982-1996.";
RL   J. Med. Virol. 51:273-279(1997).
DR   EMBL; U68694; AAB53590.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein.
FT   NON_TER       1      1
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;


  Query Match             100.0%;  Score 102;  DB 14;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db     36 PYKELRLEVGKQRLKYAQEE 55


RESULT  12
O39870
ID   O39870      PRELIMINARY;      PRT;    56 AA.
AC   O39870;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENT).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=406808;
RX   MEDLINE=97247817; PubMed=9093940;
RA   Taylor M.B.;
RT   "Molecular epidemiology of South African strains of hepatitis A virus:
RT   1982-1996.";
RL   J. Med. Virol. 51:273-279(1997).
DR   EMBL; U68695; AAB53591.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein.
FT   NON_TER       1      1
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6642 MW;  465CF51846AEF4BC CRC64;


  Query Match             100.0%;  Score 102;  DB 14;  Length 56;
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db     36 PYKELRLEVGKQRLKYAQEE 55


RESULT  13
O39871
ID   O39871      PRELIMINARY;      PRT;    56 AA.
AC   O39871;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENT).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=923359;
RX   MEDLINE=97247817; PubMed=9093940;
RA   Taylor M.B.;
RT   "Molecular epidemiology of South African strains of hepatitis A virus:
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RT   1982-1996.";
RL   J. Med. Virol. 51:273-279(1997).
DR   EMBL; U68696; AAB53592.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein.
FT   NON_TER       1      1
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6642 MW;  465CF51846AEF4BC CRC64;


  Query Match            100.0%;  Score 102;  DB 14;  Length 56;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db     36 PYKELRLEVGKQRLKYAQEE 55


RESULT  14
O39872
ID   O39872      PRELIMINARY;      PRT;    56 AA.
AC   O39872;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENT).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VDM;
RX   MEDLINE=97247817; PubMed=9093940;
RA   Taylor M.B.;
RT   "Molecular epidemiology of South African strains of hepatitis A virus:
RT   1982-1996.";
RL   J. Med. Virol. 51:273-279(1997).
DR   EMBL; U68697; AAB53593.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein.
FT   NON_TER       1      1
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6642 MW;  465CF51846AEF4BC CRC64;


  Query Match            100.0%;  Score 102;  DB 14;  Length 56;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db     36 PYKELRLEVGKQRLKYAQEE 55


RESULT  15
O39873
ID   O39873      PRELIMINARY;      PRT;    56 AA.
AC   O39873;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POLYPROTEIN (FRAGMENT).
OS   Hepatitis A virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC   Hepatovirus.
OX   NCBI_TaxID=12092;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=2333;
RX   MEDLINE=97247817; PubMed=9093940;
RA   Taylor M.B.;
RT   "Molecular epidemiology of South African strains of hepatitis A virus:
RT   1982-1996.";
RL   J. Med. Virol. 51:273-279(1997).
DR   EMBL; U68698; AAB53594.1; -.
DR   INTERPRO; IPR000886; -.
DR   PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW   Polyprotein.
FT   NON_TER       1      1
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6614 MW;  8438C51846AEF4A4 CRC64;


  Query Match            100.0%;  Score 102;  DB 14;  Length 56;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 PYKELRLEVGKQRLKYAQEE 20
          ||||||||||||||||||||
Db     36 PYKELRLEVGKQRLKYAQEE 55


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Job time: 568 sec
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